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- useful in mediating plant restrictly, espectains as a second of the se	New nucleic acid encoding a Ms45 male tissue-preferred regulatory region	WPI; 1999-105628/09.		albertsen MC. Fox TW, Garnaat CW, Huffman GA, Kendall TL;	(PION-) PIONEER HI-BRED INT INC.	23-JUN-1997; 97US-00880499.	19-JUN-1998; 98WO-US012895.	30-DEC-1998.	WO9859061-A1.	Zea mays.	Ms45; male; tissue-preferred; regulatory region; plant cells; plant tissue; differentiated; maize; hybrid seed; fertility; ss.	Zea mays Ms45 male tissue-preferred regulatory region.	08-JUN-1999 (first entry)	AAX07408;	Л 1 408 AAX07408 standard; DNA; 1394 BP.

Claim 2; Page 22-23; 39pp; English.

The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producting exogenous genes in a male tissue-preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile

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                                                The sequence is that encoding an M845 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably M845), which encodes a produce selected from auxins, rolB and diptheria coxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants
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Query Match
Best Local Similarity
Matches 1311; Conserv

100.0%; ilarity 100.0%; Conservative 0

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Indels Length 1394;

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Gaps

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Score 1311; DB 2; Pred. No. 1.2e-269; Mismatches

DB 2;

Sequence 1394 BP; 411 A; 309

C; 232 G; 442 T;

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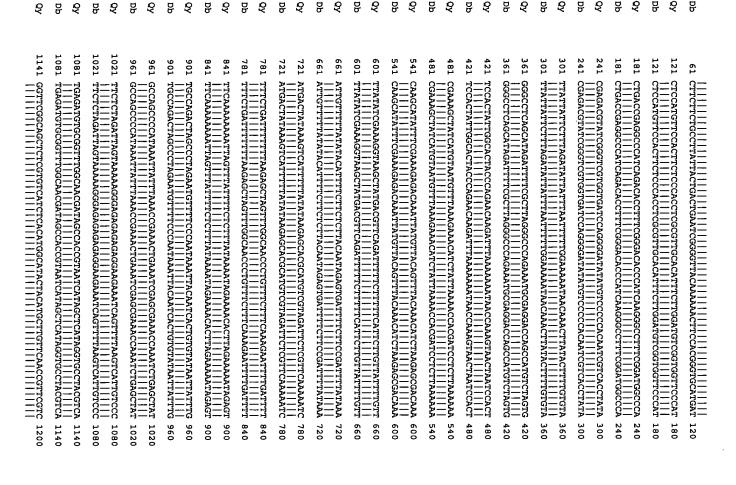
	:	
Db 1 CCATGGTGTCTTATGAAAAAGATGAGTTACAAAAAACTTCCACGGGGGCATGAT 120	· <del>-</del> -	TTCTCTAGATTAGTAA
Best Local Similarity 100.0% Matches 1311; Conservative		961 GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020 
Sequence 1394 BP; 411 A; 311 ( Query Match 100.0%;	ro N	901 TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTG 960 
impacts male tertility of exogenous gene. A method present sequence representissue preferred regula	 18888	
comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene promoter operably linked to (I) into a plant where the exogenous gene	0000	781 TTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTC
Claim 4; Page 46; 50pp; The invention provides a	O × 17 ×	721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC 780
x A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.	 × ਯਾ ਯਾ ਖ਼	661 ATTGTTTTTATATACAITTTCTTCTCTTTACAATAGAGTGATTTTCTTCCGATTTTATAAA 720 
Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL; X R WPI; 2001-514772/56.		
ON-) PIONEER HI-BRED	יי א טי א	CAAGCATATTTCGAAAGAGACAACTTATGTTACAATTTACAAACATCTAAGAGCGACAAA
FEB-2001;	ל מי א ני	481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA 540 541 CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAA 600
AUG-2001.		CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAAACCACGATCCTCTTAAAAAA
3 Zea mays. K K W0200160997-A2.	<b></b>	421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACT 480
; male tissue; regulato		
AMH/0332;  C 29-OCT-2001 (first entry)  Z mays Ms45 male tissue-preferred regulatory region encoding DNA.		
RESULT 3 AAH76332 ID AAH76332 standard; DNA; 1394 BP. XX XX XX XX	. X II & R	
1261 CCATCTTACTCATGCAACT	Db &	
1201 TIGITICAN COLCANOCTI TO CONTROLLING THE TIGITICAN COLAGA CANACCAAGA COLCANA CAACAAC TACTOCANA CAACAAC TACTOCANA CAACAAC CAACAAC TACTOCATA CAACAAC CAACAAC CAACAAC CAACAAC TACTOCATA CAACAAC CAACAAC CAACAAC TACTOCATA CAACAAC TACTOCATA CAACAAC TACTOCATA CAACAAC CAACAAC TACTOCATA CAACAAC TACTOCATA CAACAAC TACTOCATA CAACAAC TACTOCATA CAACAACAACAACAACAACAACAACAACAACAACAACA	S B S	CTCCAT
1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGLATACTACATGCTTGTCAACCGTTCGTC  1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTTCGTC  1141 GGTTCGGCAGCTCTCGTGTCATTCTCACATGGCATACATGCTTGTTCAACCGTTCGTC  1141 GGTTCGGCAGCTCTTCTCATTCTCACATGGCATACCATGCTTGTCAACCAAC	od QV	GCCTTANTTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT GCCTTANTTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT GCCTTANTTACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT
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                                                                                                                                                    Query Match
Best Local S
Matches 1311
                                                                                                                                                                                                                        The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 matissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                               A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.

    mays Ms45 male tissue-preferred regulatory region encoding

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                                                                                                                                                                                                    Sequence 1394 BP; 411 A; 309
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                                                                                                                                                                 Local Similarity
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CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120
                                                                                                                CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                   CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fox TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory region; transcription; male fertility;
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                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garnaat
                                                                                                                                                     0,
                                                                                                                                                                                                    C; 232 G; 442 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                               Score 1311; DB 5;
Pred. No. 1.2e-269;
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                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huffman
                                                                                                                                                                                                                                                                                                                                                                                          comprising nucleotide sequences the MS45 gene useful for
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1201 TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT	1141 GGTTCGGCAGCTCTCGTGTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC	1081 TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA			901 TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTTG	841 TICAAAAAAATTAGTITATITTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT 	781 TTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTGATTTT 	721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC	661 ATTGTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA	601 TTATATCGAAAGGTAGGCGTTCAGATTTTTCTTTTCATTCTTGTTATTTTGTT		481 CAAGCATATCATGTAAAGACAAAATTATGTTTAAAACAACATCTAGAACATCTAAAAAGCATCCAAAAAAA	481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAAACCACGATCCTCTTAAAAAA	421 TCCACTATTGGCACTACCCAGAACAAGATTAAAAAAATAACCAAGTAACTAATCACTATTGGCACTACTACCCAGAACAAGATTAAAAAAAA		GGGCCTCAGCA	301 TTATTATTCTTTAGATATTAATTTTTGGAAAAATAACAAACTTATACTTTTGGTA 301 TTATTATTCTTTAGATATTTAATTTTTTGGAAAAATAACAAACTTATACTTTTTGGTA		241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCCACAATCGTCACCTATA	181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA
ACTCCCAAACAAT 1260 AAH76334 Standa:             XX ACTCCCAAACAAT 1260 XC AAH76334;	1200	1140 Qy 1265	1080 Qy 1205 T	1020 MACCIES 1021 1020 QY 1145	960 SQ Sequence 25 960 Query Match Best Local Sim	900 CC CC	AATTITGATITT 840 CC comprising nucleotide sequer	780 PS XX CC CC	720 Ax male ti 720 PT A male ti 720 PT essential PT mediating	PI Albertsen MC, XX DR WPI; 2001-51477	600 XX (PION-) PIONE	540 AX PF 13-FEB-2001; 600 XX	540 XX PD	ACTAATCCACT 480 OS Zea mays. ACTAATCCACT 480 PN W0200160997-A2.	420 KW Ms45; male ti KW hybrid seed;	420 DE Z. mays Ms45	360 DT 29-OCT-2001	300 ID	300	240 Qy 1261 240 Db. 4 (41261
ird; DNA; 158 BP.	CATGCAACTTCCATGGAAAGAGGGAGATATGTTTCC LUMMG 1/1	CAACTTC	CCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCAT 1264	COTGTCATCAATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGT 12	12.3%; 97.6%;	producing hybra a Z. mays Ms45	ectide sequences essential for initiating transcription of method of mediating male fertility in a plant is nvolves introducing an expression vector comprising a ly linked to (I) into a plant where the exogenous generally linked to (E) into a plant where the exogenous generally	8; 50pp; English. provides a male tissue-preferred regulatory region (1)	<pre>ssue-preferred regulatory region comprising nucleotide sequences for initiating transcription of the MS45 gene useful for fertility in a male plant.</pre>	FOX TW, Garnaat CW, HIRIMAN G, ROHMALL LU; 2/56.	T INC.	2001WO-US004527.			<pre>ssue; regulatory region; transcription; male fertility; promoter; ds.</pre>	promoter fragment.	(first entry)	d, DNA, 255 BP.		CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
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plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
                                                     Plant full length insert polynucleotide segid 23340.
                                                                                                             ADX48600;
                                                                                                                                     ADX48600 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 47; 50pp; English
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                                                                                                                                                                                                                                                              CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 41 A;
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                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                 11.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                          50 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garnaat
                                                                                                                                                                                                                                                                                                                                                                    Score 146; DB
Pred. No. 1.7e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          21 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                           46
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                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
.7e-21;
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                                                                                                                                                                                        Matches
                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LIUJ/)
(ZHOU/)
(KOVA/)
(SCRE/)
(TABA/)
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05-NOV-2001;
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                                                                                                                                                                                                                                                   Sequence 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a recombinant DNA construct comprising polynucleotide consisting of a sequence encoding an amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    improving yield
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                                                                                                                         62
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SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    content; gene; ss.
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                                                         ATTAGTTTATTTTCTTTGAGAAAATAGAATTCCCTTGGGAAATTAGAGTTTCTAAACGA
                                                                                          ATTAGTTTATTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTA 910
                                                                                                                                                     TTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTCAAAAAAA
GCCCTTAATT 191
                           GCCCTAGAAT 920
                                                                                                                       TTTTTAGGGCTAGTTTGGAAATCTCATTTTTTCAAGAGATTTTTATTTTCCTAAAGGAA
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                                                                                                                                                                                                                                                   A;
                                                                                                                                                                                                     5.6%;
73.1%;
                                                                                                                                                                                                                                                    53 C;
                                                                                                                                                                                        0,
                                                                                                                                                                                      Score 74; DB 13; 1
Pred. No. 4.6e-06;
0; Mismatches 35;
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                                                                                                                                                                                                                                                      G; 112
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sequence
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RESULT 8
ADX33444
                                                                                        The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence consisting of a sequence encoding an amino acid sequence consisting from the US patent office at cavailable in electronic form from the US patent office at the property of the invention are also useful in physical arrays of molecules and as confirmed and the invention are also useful in physical arrays of molecules and as comproving plant tolerance to cold, heat, drought, herbicides, extreme commonic conditions, pathogens or pests, for manipulating growth rate in commonic conditions, pathogens or pests, for manipulating growth rate in conserving continuous, pathogens or pests, for manipulating growth rate in content cells by modification of the cell cycle pathway, for conferring contrassed resistance to plant disease, for producing galactomannan, configurate, for improving the rate of homologous concentration in plants, for improving yield by modification of cor modifying seed oil or phosphorus use and/or uptake cor by providing improved plant growth and development under at least one content. This sequence represents a plant full length insert content. This sequence represents a plant full length insert content of the underly content of the content of the content of the content of the content of the
Query Match
Best Local S
Matches 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LIUJ/) LIU J.
(ZHOU/) ZHOU Y.
(KOVA/) KOVALIC D K.
(SCRE/) SCREEN S E.
(TABA/) TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant full length insert polynucleotide segid 16264.
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05-NOV-2001; 2001US-00985678.
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                        Similarity
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        Score 74; DB 13;
Pred. No. 5.4e-06;
0; Mismatches 35
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                                                                                             G; 189 T; 0 U; 0 Other;
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   plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; hat tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; extreme commotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the sequence period of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme semotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring lightn or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of
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05-NOV-2001; 2001US-00985678.
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yield; plant growth; plan
protein content; gene; ss
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                                                                                                                                                                                                            Claim 1; SEQ ID NO 32493; 15pp; English.
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ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; heatbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2445 BP;
  Claim 1; SEQ ID NO 17816; 15pp; English
                                           pests, for conferring improving yield.
                                                                            New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                            (LIUJ/)
(ZHOU/)
(KOVA/)
(SCRE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADX34996 standard; cDNA; 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-2001;
                                                                                                                                                                                                                                                                                              (CAOY/)
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                                                                                                                                                                                                                                                                                                                      KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                   LIU J.
                                                                                                                                                                                                                                                                                              CAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                          Zhou Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCCTAGAATGTTTTCCCAATAAA 934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTAGGGCTAGTTTGAGAACCCTTTTTTTTCCCAAAAGATTTTCATTTTTCAAAGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTAGTTTATTTTCTCTTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCCTTAATGTTTTTTTTCATGAA 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003US-00425114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-00985678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00304517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene;
                                                                                                                                                                                                                                          Kovalic
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73.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.
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Pred. No. 1
                                                                                                                                                                                                                                             Screen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         513 G; 796
                                                                                                                                                                                                                                          SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4e-05;
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                                                                                                                                                                                                                                          Tabaska JE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 Other;
                                                                                                                                                                                                                                             Cao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a recombinant DNA construct comprising a conjunct consisting of a sequence encoding an amino acid sequence convaliable in electronic form from the US patent office at the sequence encoding an amino acid sequence conjunction are also useful in physical arrays of molecules and as conjunction are also useful in physical arrays of molecules and as comparing plant tolerance to cold, heat, drought, herbicides, extreme comparing plant tolerance to cold, heat, drought, herbicides, extreme commetic conditions, pathogens or pests, for manipulating growth rate in creased resistance to plant disease, for manipulating growth rate in concreased resistance to plant disease, for producing galactomannan, concreased resistance to plant disease, for producing galactomannan, conformation in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake cordition or plant growth plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert conjuncted that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                   recombination was considered, drought tolerance; herbicide cold tolerance; heat tolerance; drought tolerance; herbicide cold tolerance; heat tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; galactomannan production; lignin production; plant growth regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 928
                 (LIUJ/)
(ZHOU/)
(KOVA/)
                                                                                      06-MAY-1999;
05-NOV-2001;
                                                                                                                                                                                                           US2004034888-A1
                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                             plant protectant; plant growth regulant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADX61114
                                                                                                                                        28-APR-2003; 2003US-00425114
                                                                                                                                                                           19-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                               recombinant DNA
   (SCRE/)
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                                                                                                                                                                                                                                                                         plant growth; plant development; n content; gene; ss.
                   ZHOU Y.
KOVALIC D
                                                      LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                      99US-00304517
2001US-00985678
                                                                                                                                                                                                                                                                                                                                                              t; plant growth regulant; gene therapy; plant;
construct; physical array; plant breeding marker;
heat tolerance; drought tolerance; herbicide tolerance;
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78.0%;
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Pred. No. 1.8e
0; Mismatches
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L.8e-05;
hes 27;
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RESULT 12
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Best Local Sir
Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or peets, for conferring increased resistance to plant disease, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TABA/)
(CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 31957; 15pp; English
                                                                                                                                     plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance, herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance;
                                                          galactomannan production; lignin production; yield; plant growth; plant development; seed protein content; gene; ss.
                                                                                                                                                                                                                                                                          Plant full length insert polynucleotide seqid 31061.
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                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                    ADX60218 standard; cDNA; 3607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTTAATGTTTTTTTCATGAA 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTAGAATGTTTTCCCAATAAA 934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTAGGGCTAGTTTGAGAACCCCT-TTTTTCCCAAAAGATTTTCATTTTTCAAAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 685 A; 484 C; 524 G; 844 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71.8; DB
Pred. No. 2.2e-(
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
2.2e-05;
les 37;
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                                                                                       plant growth regulator;
oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2537;
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RESULT 13
AAL15210/c
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Best Local Sim
Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                       osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ttp.seqdata.uspto.gov/sequence.html?DocID:200403488. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004034888-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 31061; 15pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-180133/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu J,
                                                                                                                                                                                                                                                                                                                                                                  Sequence 3607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SCRE/)
                                        AAL15210;
                                                                  AAL15210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              improving yield.
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                                                                                                                                                                                                                                                                                                                                                                                               nvention
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TABASKA J E
CAO Y.
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                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                        TTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAG
                                                                                                                                                                                                                                                      TCTTÁGGGCTÁGTTTGAGAÁCCCT-TTTTTCCCAÁAAGÁTTTTTCATTTTTCAAAGAAAAA
                                                                                                                                                              CCCTAGAATGTTTTCCCAATAAA 934
                                                                                                                                                                                              standard;
                                                                                                                                         CCCTTAATGTTTTTTTTCATGAA
                                                                                                                                                                                                                                                                                                       5.5%;
milarity 73.4%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                    BP;
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                                                                                                                                                                                                                                                                                                                                                                    915 A; 695 C; 718 G; 1279 T; 0 U; 0 Other;
                                                                     cDNA;
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0; Mismatches
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                            DB 13;
                                                                                                                                                                                                                                                                                                                37;
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                                                                                                                                                                                                                                                                                                                                            Length 3607;
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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09-JUN-2000;
25-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is affilicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded potentially preventing breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JAN-2000;
14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide useful as a marker for the diagnosis of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAR-2000;
29-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides are also useful for isolating activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lillie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200151628-A2
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513
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AAAAAAATTTTTTNAAANTNTTTTTAAAAACCTTNAATTNAAANANAATTTTTTTNNNTT
                  AAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAA
                                                                                                         AATTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTG
                                                                                                                                                                                                                  TTAAANNTTTTNTAANTTATTAAACCAAAATTTTTTTTTAAAAAAATTTTTTAAAANTT
                                                                                                                                                                                                                                             AACAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACA
                                                                                                                                                                                                                                                                      TANAAATTTTTTNAAAAACTAATTNTAANNATANTNAATTTTTTNTAAAAAANNNAAAAA
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                                                                                                                                                                                                                                                                                                                                                      TGTCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCA
                                                                                                                                    TTATTGTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATA
                                                                                                                                                              <u>AATAANTTNAATTTTTTTTTAATNAAAAAAAAAATTTNAAATTTTAANCAANTNTTTTTT</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0176077P.
2000US-0189167P.
2000US-0192099P.
2000US-0193480P.
2000US-0205230P.
2000US-0201315P.
2000US-0220534P.
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3695pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               5.4%;
39.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell marker; cytostatic; ss
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 70.2; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                        23 G; 396 T; 0 U; 124 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide 7667.
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compounds with
                                                                                                                                                                                                                                                                                                                                                                                                            Length 883
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Best Local Similarity Matches 237; Conserv

Conservative

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Mismatches

Indels Length

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Gaps

5.4%; 39.2%;

Score 70.2; DB 11; Pred. No. 3.9e-05;

Query Match

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RESULT 14
ACN85231/c
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                      The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN85231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breast cancer related marker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACN85231
Sequence
                                                                                                                                                                                                                                                                      Novel isolated polypeptide associated with breast cancer, detecting presence of polypeptide in sample, as a marker i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003099974-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer; breast;
                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                               18-JUL-2001; 2001US-0306220P
                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUL-2002; 2002US-00198846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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960 BP;
                                                                                                                                                                                                                            SEQ ID NO 6381; 36pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour; cytostatic; marker; detection; therapy; ds.
340 A; 33 C; 39 G;
                                                                                                                                                                                                                                                                                                                                                   Wang
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 421 T; 0 U; 127 Other;
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flowering locus T gene; FT; terminal flower; TFL; Apetala3; Ap3; plant; floral development; plant sterility; plant fertility; flowering time; plant growth rate; inflorescence architecture; tissue culture morphology; cell division; FT homologue; gene; ds.
Danilevskaya O, Hermon P, Bruggemann E, Shirbroun D, Rafalski JA, Sakai H, Cahoon E, Cahoon R, Klein T;
                                                                                                                      30-JAN-2003; 2003US-00343477.
                                                                                                                                                            29-JAN-2004; 2004WO-US002422
                                                                                                                                                                                                         12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                  Corn FT homologue nucleotide sequence SEQ ID NO:63.
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                                                            (DUPO ) DU PONT DE NEMOURS & CO E I.
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WPI; 2004-580996/56
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New polynucleotides, specifically nucleic acid fragments encoding flowering locus T gene (FT) or terminal flower (TFL), or Apetala3 (Ap3) homologs, useful for floral development, e.g. engineering plant flowering

Claim 6; SEQ ID NO 63; 109pp; English.

Crist, second, third, fourth or fifth nucleotide sequence, or their complement encoding a polypeptide either having flowering locus T gene (FT), terminal flower (TFL), or Apetala (Ap3) homologue activity. Also construct; comprising the polynucleotide; (2) a recombinant DNA construct; comprising the polynucleotide; (3) a recombinant CC DNA construct; comprising the polynucleotide; (4) a cell comprising the cell with the polynucleotide; (3) transforming a plant from the creombinant DNA construct; (5) producing a plant comprising transforming (CC a plant cell with the polynucleotide, and regenerating a plant from the creombinant DNA construct; (6) a plant comprising the recombinant DNA construct; (8) an isolated polynucleotide comprising the recombinant DNA construct; (8) an construct; (7) a seed comprising the recombinant DNA construct; (8) an construct is comprising the recombinant DNA construct; (8) an isolated polynucleotide sequence contains at least 30 nucleotides, and where the crist nucleotide sequence; (9) an isolated polyputide having FT or Ap3 construct polynucleotide comprising isolating a polypeptide encoded by the polynucleotide comprising isolating the polynucleotide comprising isolating the polynucleotide comprising the polypeptide from a cell containing a recombinant DNA construct comprising the polynucleotide comprably linked to a regulatory sequence. The polynucleotide ere useful construct polynucleotide comprising the polypeptide from a cell construct polynucleotide comprising the polynucleotide comprising the polypeptide are useful construct morphology and the rate of cell division to enhance contained the rate of cell division to enhance contained the present sequence represents an FT homologue contained the present invention.

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Sequence 13400 BP; 3962 A; 2948 C; 2695 G; 3795 T; 0 U; 0 Other;

Matches 89; Query Match Best Local ( 1 5.3%; Similarity 73.6%; 39; Conservative ( 0; Mismatches Score 69.8; DB 13; Length 13400; Pred. No. 9e-05; 32; Indels 0; Gaps

Ş B Ş 8619 AAAAATAAAAATCCATTAGAAAATGGGGTTGTCAAACTAGTCCTTATTTAGTTTTCCAT 8678 871 TAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCTAGAATGTTTTTCCCAA 930 931 T 931

8559 ACCATTTTATTTTCAAGAGGTTTTTTTTTTTTTTATCAAGAAAAATTAGTTCATTTTCTCTTGG 8618

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Search completed: March Job time: 875.437 secs 5, 2006, 18:11:32

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## ALIGNMENTS

Query Best Match	ORIGIN	FEATURES sou			JOURNAL	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BD062176 LOCUS DEFINITION
Query Match 100.0%; Score 1311; Best Local Similarity 100.0%; Pred. No. 7. Matches 1311; Conservative 0; Mismatches		Location/Qua	PI TIMMY I KANUALLI PC (212N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC C07K14/34,C12Q1/68, PC A01H5/00 PC A01H5/00 CC Strandedness: Single; CC Strandedness: Single; CC Topology: Linear; PU Volume (Constitution (Con	PD 30-0CY-2001  PF 19-JUN-1998 JP 1999504910  PR 23-JUN-1997 US 08/880499  PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMAN,	AL		SW 2	1 76 BD062176 1394 bp DNA linear TON MEDICATION PROFESTION AND PRO
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1 (bases 1 to 1394)
Ribertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and
                                                                                                                                                                                       CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
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                                                                           CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT
                                                                                                                                              CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAAACTTCCACGGGTGCATGAT
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                                                            CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT
                                                                                                                           CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT
CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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601 TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTCATTCTTGTTATTTTGTT	B &		CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTT
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481 CGAAAGCTATCATGTAATGTTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA	Db Qy	<del></del>	1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC 1200
421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAATAACCAAAGTAACTAATCCACT 	B &		1081 TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA 1140
361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG	dd VQ	<del></del>	1021 TTCTCTAGATTAGTAAAAAGGGAGAGAGAAGAAATCAGTTTTAAGTCATTGTCCC 1080
301 TTATTATTCTTTAGATATTATTTAATTTTTTGGAAAATAACAAACTTATACTTTTGTOTA 	т. В 89		961 GCCAGCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020 
241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA	, B &		901 TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAAATTATTTG 960 
181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA	DD QY		841 TTCAABAAAAATTAGTTTATTTTCTCTTTATAAAATAGBAAAACACTTAGBAAAAAATAGAGT 900
121 CTCCATGTTCCACTTCTCCCACCTGGGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT	B Q		781 TTTCTGAITTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAAITTTGAITTT 840
61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAACTTCCACGGGTGCATGAT	B 6		721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGGTTCAAAAATC 780
1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC	B 6	•	661 ATTGTTTTATATACATTTTCTTCTCTACAATAGAGTGATTTTCTTCCGATTTTATAAA 720
Query Match 100.0%; Score 1311; DB 6; Best Local Similarity 100.0%; Pred. No. 7.2e-228; Matches 1311; Conservative 0; Mismatches 0;	3 m O		601 TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT 660
/mol_type="u /db_xref="ta	ORIGIN		541 CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAA 600 
o O	FEA		481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA 540
REFERENCE 1 AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L. TITLE Male tissue-preferred regulatory region and method of using same JOURNAL Patent: WO 0160997-A 1 23-AUG-2001;	RER REF		421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACT 480
MSIN	0		361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG 420
ION AX224394 N AX224394.1 GI:155546 DS 755 mays	ACCESS VERSIO KEYWOR		301 TTATTATTCTTTAGATATTAATTTTAATTTTTGGAAAAATAACAAACTTATACTTTTGTGTA 360 
RESULT 3.  AX224394 1394 bp DEFINITION Sequence 1 from Patent WOO160997.	RESUL AX224 LOCUS DEFIN	(8) 11	241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCCACAATCGTCACCTATA 300,

Query Match Best Local: Matches 131	TITLE JOURNAL FEATURES BOUIC ORIGIN	SOURCE ORGANISM ORGANISM REFERENCE	RESULT 4 AX224395 LOCUS DEFINITION ACCESSION VERSION	D Q	B &	Db Qy	Db Qy	B &	Db Qy	Qy db	dy Qy	Qy dd	φ φ	Db
uery Match 100.0%; Score 1311; DB 6; Length 1394; est Local Similarity 100.0%; Pred. No. 7.2e-228; atches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	Alberteen, M.C., Fox, T.W., Garnast, C.W., Huffman, G. and Kendall, T.L. Male tissue-preferred regulatory region and method of using same Patent: WO 0160997-A 2 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US) Location/Qualifiers 1. 1394 /organism="Zea mays" /mol type="unassigned DNA" /db_xref="taxon:4577"	Zea mays  Zea mays  Zea mays  Eukaryota; Viridiplantae; Streptophyta; Embryophyta  Spermatophyta; Magnollophyta; Lillopsida; Poales; I  clade; Panicoideae; Andropogoneae; Zea.	AX224395 1394 bp DNA linear PAT 10-SEP-2001 N Sequence 2 from Patent WO0160997. AX224395 AX224395.1 GI:15554637	1261 CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311	1201 TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260	1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC 1200 	1081 TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA 1140	1021 TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAGAAGAAATCAGTTTTAAGTCATTGTCCC 1080	961 GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020 	901 TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAAATTATTTG 960 	841 TTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT 900 	781 TITCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTC	721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGGTTCAAAAATC 780	661 ATTGTTTTATATACATTTTCTCTCTACAAFAGAGTGATTTTCTTCCGATTTTATAAA 720
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1021 TICTUTALATTRIGTAAAAAGAAGAAGAAAAATCAGTTTTAAGTCATTGTCCC 1080 1081 TGAGATTGTGGGGAAGAAGAAGAAATCAGTTTTTAAGTCATTGTCCC 1140	Ş B	Query Match 100.0%; Score 1311; DB 15; Length 3343; Beet Local Similarity 100.0%; Pred. No. 6.2e-228; Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1021 TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAGAGAAGCAAATCAGTTTTAAGTCATTGTCCC 1080	ν,		
961 GCCAGCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020 961 GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020	D Q	RIMRYWLEGPRAGEVEVFANLPGFPDNVRSNGRGOFWVAIDCCRTPAQEVFAKRPWLR TLYFKFPLSLKVLTWKAARRWHTVLALLDGEGRVVEVLEDRGHEVMKLVSEVREVGRK LWIGTVAHNHIATIPYPLED"	
TGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTAGTTTG	Db	DGRVVRWIGEESGWEI'F AVWIPUWSESVCANGVWSI TRACHESE CARK JALLE TOLLE T	
901 TGCCAGACTAGACTTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTG 960	Q	/translation="MEKRNIQWRRGRDGIVQYPHLFFAALALALLVADPFGLSPLAEV DYRPVKHELAPYGEVRGSWPRDNASHLRRGRLEFVGEVFGFES IEFDLOGRGFYAGLA DYRPVKHELAPYGEVRGSWPRDNASHLRRGRLEFVGEVFGFES IEFDLOGRGFYAGLA	
641 TTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT 900	B 8	/COURTE STATE AT THE PROPERTY OF THE PROPERTY	
781 TTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAAT111GA111 070	D Q	/product="male fertility protein" CDS	
ATAAAGTCATTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC	Db	mRNA join(<13921768,18982182,22802447,2534>2942) /dene="Ms45"	
721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC 780	Q	gene (1392 - 2942 Jene="M945"	
661 ATTGTTTTATATACATTTCTTCTTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA 720	da	/CLITAVAT="B/3"  /db_ref="text="4577"  /brencene_HOT"	
661 ATTGTTTTTATATACATTTTCTTCTCTTACAATACAGTGATTTTCTTCCCGATTTTATAAA 720	8	. ~ ~	
	р, ;	PEATURES 13343  BOUICE 13343	
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481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAAACCACCATCCTCTTAAAAAA 540	D Q	Fox, T.W., Cloning of Unpublishe	
TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACT	Db st	Eukaryota; Virioiplantae; Streptophyta; Embryophyta; Iradheophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  PEFERPINCE 1 (bases 1 to 3343)	
361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG 420 421 TCCACTATTCGCACTACCCAGAACAAGAAAAAAAAAAAA	9 B	Zea mays SM Zea mays	
	Q	ACCESSION AF360356 VERSION AF360356.1 GI:14028756 KEYMORDS	
301 TTATTATTCTTTAGATATTAATTTAATTTTGGAAAAATAACAAACTTATAACTTTTTGGTA 360	g Qy	AF360356  AF360356  AF360356  DEFINITION Zea mays male fertility protein (Ms45) gene, complete cds.	
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241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCCACAATCGTCACCTATA 300	Q	1261 CCATCTTACTCATGCAACTTCCATGCAACACACGCACATATGTTTCCTGAAC	
181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGGATGGCCCA 240	문 원	Db 1201 TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260 Ov 1261 CCATCTTACTCATGCAACTTCCATGCAAACAGCGCACATATGTTTCCTGAAC 1311	
CTCCATG	D D	CTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT	
	<i>i</i> , , , , , , , , , , , , , , , , , , ,	1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACATGCTTGTTCAACCGTTCGTC	
61 CTTCTTCTGCTTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120		Db 1081 TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA 1140 Ov 1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC 1200.	
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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/mol_type="unassigned
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Schubert,K., SanMiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T.,
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                                                                                                                                                          Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. a
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3 (bases 1 to 188283)
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NOTE: This is a 'working draft' sequence. It currentl consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record arbitrary. Gaps between the contigs are represented a runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGTCATCTCACATGCATACTACATGCTTGTTCAACCGTTCGTCTTTGTTCCATCGTC
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                                                                                                         Web site: http://www.tigr.org/tdb/tgi/maize/Contact: maize@tigr.org
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	Direct Submission	Vassiliev,H., Venkataraman,v.S., viel,k., vo,A., wilsou,b., mu,A., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.	Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,	Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,F., Smitti,C., Spencer.B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,	Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,	O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,	Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,	Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,	Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,K.,	Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,	Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,	Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,	Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,	Anderson,M., Arachchi,H.M., Barna,N., Babtien,Y., Brown,i., Choepel,Y.,	Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,	Unpublished	Zea mays, clone ZMMBBc0334A01	Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, K., Bhaiti, A.K.		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACLAD	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Zea mays	Ħ	AC147602.5 GI:51315585	ces.	R	106100 h				909 TAGCCCTA 916	70 AAATTAGTTTATTTTTCATAGTAAAATAGAAATCTCTTAGAAAAATATAGTTUUCAAAU 35829		777777	TTGTTTAA	789 TITTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTTGATTTTTTCAAAAA 848	rvative (	/ Match 5.9%; Score 77.2; DB 14; Length 188283;			/escimaced_rengcn=unknown 184424184523	173245 173344	/estimated_length=unknown	/estimated_length=unknown	167406. 167505	162086162185 /estimated length=unknown	/estimated_length=unknown	C	159717159816	

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This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Q20 or manually edited. This assembly was performed with Arachne (Genome Res. 2002 12: 177-189; Genome Res. 2003 13: 91-96). All trace files for this project are available at the NCBI trace repository (http://www.ncbi.nlm.nih.gov/Traces/trace.fcgi?). An exact list of reads used in this assembly are available at http://www.broad.mit.edu/annotation/plants/maize/randomclones.html.
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Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box, 210088, University of Arizona,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (17-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 17, 2004 this sequence version replaced gi:49658659. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced to the continuous contin
by the finished sequence as soon as it is available and the accession number will be preserved.

1 100617: contig of 100617 bp in length 100618 100717: gap of unknown length 100718 104730: contig of 4013 bp in length
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Center clone name: 334_A_1
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Center code: WIBR
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                                                                                                   Submitted (24-FEB-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquirities: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 26, 2005 this sequence version replaced g1:60279457.
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                               CR936840 161616 bp
Danio rerio clone DKEY-91021, ***
                Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
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Danio rerio (zebrafish)
Center project
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100618. .100717
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115104: contig of 10274 bp in length
115204: gap of unknown length
156396: contig of 41192 bp in length
156396: gap of unknown length
179396: contig of 23440 bp in length
180036: gap of unknown length
186199: contig of 6163 bp in length.
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name: zK91021
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Insert size: 160313; 4.7% error; aggarose-fp
Quality coverage: 6.55x in Q20 bases; sum-of-contigs Quality
coverage: 6.56x in Q20 bases; agarose-fp
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mol_type="genomic DNA"
note="assembly_fragment:00794
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ragment_chain:1"
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3258: gap of 100 bp.
11860: contig of 8602 bp in length
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ORGANISM
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VERSION
KEYWORDS
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                                                                                                   REMARI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79551 ATATATATATATATATATTTTT 79574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               876 ТАБААЛАСАСТТАБАЛАЛАТАБАБТТБСССАБАСТАБСССТАБАТСТТТТССССАЛТАЛАТ 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                816 GTTTCTTTCAAAGAATTTTGATTTTTTCAAAAAAAATTAGTTTATTTTTCTCTTTTATAAAA 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 TTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAGCTATGACGTTCAGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25769 bp l
Dictyostelium discoideum chromosome
AX4, complete sequence.
AC117267 AC115507
                                                                                                                                                                                                                                        Dictyostelium discoideum
Dictyostelium discoideum
Dictyostelium discoideum
Bukaryota, Mycetzoa, Dictyosteliida; Dictyostelium.

1 (bases 1 to 25769)
1 (bases 1 to 25769)
1 (bases 1, Eichinger, L., Szafranski, K., Pachebat, J., Dear, P., Gloeckner, G., Eichinger, L., Szafranski, K., Guigo, R., Kumpf, K., Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K., Lehmann, R., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                 Direct
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                                                             the Dictyostelium Genome Sequencing Consortium (bases 1 to 25769)
                                                                                                                                                      bequence and analysis of chromosome 2 of Dictyostelium discoideum vature 418 (6893), 79-85 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCT 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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fragment_chain:1"
158891. 161616
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97494. .103542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_fragment:00074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ragment_chain:
37399. .158790
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47.9%;
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Pred. No. 0.
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:1"
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2 map 5836255-5862024 strain
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On or before Feb 21, 2004 this sequence version replaced
gi:19570016, gi:20087114.
CDS predictions from GeneID may contain errors. Further Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (21-FEB-2004) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml
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AFFTLVRHTPRNITYYKVVWGGGGVGKSAIIIQPIQNHFVEEYDFIIEDSYRKQVTIS
GLPPIGGSLMKKGSSGSSSSSSSSKYGLFMLITSGKUKQBSPQQAASPSTIDRTGQI
STNRLEANVLSYSMSNLSKEVPLITGDCVYCQGCNVILSRFSNLVKTGDDSFTWKCEF
CKYSNSNILLEQGEIPNKDSVEYVLSSPSTSSTTDGSKREESIIIYCIDVSGSMGITT
EVPSLQSEWNAKKGVKGASSGPSYJSRLECVQSIPTHOSKREESIIIYCIDVSGSMGITT
EVPSLQSEWNAKKGVKGASSGPSYJSRLECVQSSIPTHOBLSIQYBUKREVLLVFF
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EVQSTALGPALLVSAAIASQKMLSEVVICTDGVBNVGLGAIEDLFLGPAQEFYEKVT
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TDVEMSICLHFTLEINKYDSKQGLSRVWGFPBNNSLTDLTLLYSSRNRFTEFVQIYP
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PGIQIKTKLDGVRCLRVVSAQLQATDBNTSTSNANISILANAFTQQAKKLAQQGEY
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FSKQVIKSFLQNGYNIGIKSSKNTFIKIFENNKOKLFSSLFFFYLKNIAENQEFEDYY
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FSKQVIKSFN
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                                           Hypothetical protein"
/protein_id="AAS38627.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MESRLHLKAATKLIRSLCNTDEQWEEFYNFEVLREEMEAPLITCIKNKQQRVEKAATD
DEIQVFYKMKNVHKSFVEGGRKKDISRRKGEAEINKQYYNIKFT"
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join(2957. .3173,3272. .5583)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="GeneID exon scores (in order of location ranges):
68.61 - GSCJ_ID dd_00752"
/codon_start=1
KNSNHWMMPSLKINQIINDNNNNISNINFVQIQSNSSSLSSSCSTYQSCPIEDEHIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (5711. .6796)
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23.68, 1.54, 15.75, 9.21, -4.75 - GSCJ_ID dd_03387"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="5836255-5862024"
                                                                                                                                                                                                  translation="MSSRVKSLIERYNGINLTIEKSLSPRGLINTNINNNINNNNNNNN
                                                                                                                                                                                                                                                                                                                                                                                                               product="similar to Plasmodium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="GeneID exon scores (in order of location ranges):
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strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Dictyostelium discoideum"
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moldi. Spore coat protein SP87 precursor (PL3 protein)"
/protein id="AA38631.1"
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/db_xref="G1:42733683.1.1"
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/VDQHGKECCYVAHRPPFPKCSLRCPPHHECRVNHFGEECCVKVHHDKCSLRCPPGHECK
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/VDQHGKECCYVAHRPPFPKCSLRCPPKHECRINFGEECCVXSRNDCLTCEDLNCERKG
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IINANSLWIKSSIDSRNISNSFINSRCSFNBYFEKNSSDAGGPFILTIGLUCHSIQLSID
ENSIIESKEFGTINYHAKSFFLLINDLYSFNREINENDLLNYIKILAQLNSIQLSID
KTIELIIDHYLKFLSSIETILKLYQNDQSTYQLLKQVFQNGNKILSGIYFAHKKSKÄY
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23.29 - GSCJ_ID dd_00728"
/codon_start=1
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LTDAPVAASSSSSVKYTIDVLLSFKSANTKRPIQIDIVENHÖKEIVVPLSLPTTPYN
NNNNNNNNNTNNSSQHNTANGOKYPIFSPOISPKIAYAQSSTKTNINNNNNNNNNNNNT
TKKANSNITTPOSNNRNNHYNSNTKSSTKKONPIFSLNTAFPNÖKNTTTTPSKKSTT
TTPKSNKKINDVNAAFAAVANSTTTTEOPVAIIDGATPSTNESPKKTPLKETDPKRLA
ARORQIDIGKMTAGYKNYIALVPKSKRKPTDPKTPNKNOVCSKRSWOGQIKKMRRQLH
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PNNAPIKKNSVGIIGNGPNVNNNKDRKLNSNDGVNFGKKNILFTPSKNSMVSTTKHS
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QNSMSPPKLDKRRESRDLIPFIANI"
Join(8924. 9076,9236. 10573)
/note="GeneID exon scores (in order of location ranges):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFNQI I PQGI F I HTKLKSLNFGYHFNQI I PADTLPPTLESLNLGGYNRE I TVKNDEYD
CYG I SNKGGFGSNS SSNFCVGGTNNGLREMLKNTTSLKTLTLNY FNRK I EVGDLPNS I
BSLNLGYHFNQP I GNNVL PKLLKKLF I LNSEFNQN I SADGCI PFGLQT I Y I RNSNMNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="similar to Dictyostellum discoideum (Slime mold). Spore coat protein SP87 precursor (PL3 protein)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(16184. .16199,17272. .17613,17707. .19331)
/note="GeneID exon scores (in order of location 0.08, 32.32, 227.42 - GSCJ_ID dd_00726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSLNPLFITKYINIIDLSHL"
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RESULT 12
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   558 AGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAG 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498 TGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACCAAGCATATTTCGAAAG 557
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                                                                                                                                                                                                                                          TTAAAAATTGGGTGTTTGATTGAAAAATATTCTTTTAAATTTTTTCAGGAAATATCTTTT
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                                                                                                                                                                              TATTTTCTCTTTATAAAT 876
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ilarity 49.4%;
Conservative (
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EDILKUKSIKWKVOGYITRTIHRILLLACUSMDLLKSDESIMKOMSQOPDENNVIEK
SLIDERNGFAQLAQVEVLARYEDDVVWKRDYLALLETEQSMSIEYLKQQEQSKEVKNV
SSTIQFNEKLFSLLVILFYTKYEFQNQSFSFFLHSQUGVISATREEIGLGKIGDELK
YTQNYFSTLVGNFFEFFSKCKGDELAIIDSFKVYNTSSYFLTFSRSSTNFLGSSSIGHL
TIRNNSKSITATLRGQKRRSVQKGNPFSLLPLHERTFSFKGHWCFEIIDGEVNQIDVI
THREFECCHIVOLY
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/protein_id="AAS38633.1"
/db_xref="GI:42733689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHCAMKTVPIDKBNCCEKVÞVCYSNNPLLDGGHGFI"
19762: .21336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DMYNDDDKSSTSSQSSSSSSSSSSAPSSPKFIKNNDNNTTTTTTTTTTTTTTTKTATTS
LSTIEKFQVFNVDQIPEISIEAYIERVFKYLPFGTDIFIFSTIYLDRLIQMNQEIQIS
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1/3.48 - GSCU_TD dd_00724"
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rotein_id="AAS38632.1"
b_xref="GI:42733688"
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Pred. No. 0.0014;
0; Mismatches 221; Indels
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KEYWORDS
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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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AC155379.2 GI:58082241
HTG; HTGS_PHASE1.
Zea mays
Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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Seq_lib_id: ZOCF
------ Project informaton
Web_site: http://www.tigr.org/tdb/tgi/maize/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: maize@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to 172293)
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contig
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172293 bp DNA linear HTG Zea mays strain B73 clone ZMMBBb0131C15, *** SEQUENCING ***, 27 unordered pieces.
AC153379
                                          25-JAN-2005
IN PROGRESS
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1 (bases 1 to 172293)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Char, A.P., Pertea, G., Zheng, L., Cheung, F., Fraser, C.M., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. a Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Pantocideae; Andropogoneae; Zea.

1 (bases 1 to 172293)

Chan,A.P., Pertea,G., Zheng,L., Cheung,F., Lee,D., Koo,H., Utterback,T.R., Feldblyum,T.V., Rabinowicz,P., Fraser,C.M., Utterback,T.R., Samiquel,P., Ma,J., Pontaroli,A.C., Rohlfing,T., Schubert,K., Samiquel,P., Ma,J., Barbazuk,B., Bennetzen,J. and Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and

3 (bases 1 to 172293)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. a and

Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr. Rockville, MD 20850 On Jan 25, 2005 this sequence version replaced gi:57862900.

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is

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2421: contig of 2421 bp in length 2521: gap of unknown length 5334: contig of 2813 bp in length 5434: gap of unknown length 8098: contig of 2664 bp in length of unknown length
ig of 2244 bp in length
of unknown length
ig of 21042 bp in length
of unknown length
ig of 8102 bp in length
ig of 8102 bp in length
ig of 13429 bp in length
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TITLE Direct Submission  JOURNAL Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),  9712 Medical Center Dr, Rockville, MD 20850  REFERENCE 3 (bases 1 to 201985)  AUTHORS Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,  Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,  Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,  Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and		RESULT 13 AC155618/c LOCUS DEFINITION AC155618 AC155618 AC155618 AC155618 CCESSION AC155618 VERSION AC155618 VERSION AC155618 VERSION AC155618 VERSION AC155618 VERSION AC155618 CREAMORDS AC155618 VERSION AC155618 VERSION AC155618 VERSION AC155618 SOURCE Source Source Sea mays Source Sea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Elliopsida; Poales; Paccad Spermatophyta; Magnoliophyta; Liliopsida; Poales; Paccad Clade; Panicoideae; Andropogoneae; Zea.	estimated length=unknown

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FEATURES SOUICE Gap Gap Gap				TITLE JOURNAL COMMENT
* 185973 199501: contig of 13529 * 199602 199601: gap of unknown * 199602 201985: contig of 2384 Location/Qualifiers 1201985 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone="ZMMBBC0344D04" 19172016 /estimated_length=unknown 2248122580 /estimated_length=unknown 3046930568	138840 146859: contig of 8020 bp in length 146860 146959: gap of unknown length 146860 152969: contig of 6010 bp in length 152970 153069: gap of unknown length 153070 155026: contig of 1957 bp in length 155027 155126: gap of unknown length 155127 156434: contig of 1957 bp in length 15635 156534: gap of unknown length 15635 173224: contig of 16690 bp in length 173225 173324: gap of unknown length 173225 173324: gap of unknown length 173225 174858: gap of unknown length 173225 174858: contig of 1534 bp in length 174859 182700: contig of 5372 bp in length 182701 182800: gap of unknown length 182801 185972: contig of 3072 bp in length 185873 185972: contig of 10572 bp in length	78874: gap of unknown length 87797; contig of 8923 bp in 1 87897; gap of unknown length 94463; contig of 6566 bp in 1 94563; gap of unknown length 121761; contig of 67198 bp in 1 121861; gap of unknown length 124636; contig of 2775 bp in 1 124736; gap of unknown length 131029; contig of 6293 bp in 1 131029; contig of 7610 bp in 1 1318739; contig of 7610 bp in 1 138839; gap of unknown length 138839; gap of unknown length	Seq_lib_id: 2GGW  Web site: http://www.tigr.org/tdb/tgi/maize/ Contact: maize@tigr.org  Contact: maize.  Contact: maize.	5) The Institute for Genomic Research r, Rockville; MD 20850 sequence version replaced gi:57863139
				(TIGR)
	Db 44986  Qy 852  Db 44927  Qy 912  Db 44867  RESULT 14  ARCSULT 14  ACCUS LOCUS  DEFINITION P	gap gap gap oRIGIN Query Match Best Local Matches 10 Qy 792	дер дер дер дер дер дер дер дер	gap gap
ia para plexa; bacham, ,H.G. racter ers of	TATAAGG TTAGTTT TTAGTTC TTAGTTC CCCTAGA               CCCTAAA	p /estimated_length=unknown 185873185972 p /estimated_length=unknown 19502195601 p /estimated_length=unknown  / Match		/estimated_length=unknown 6521965318 /estimated_length=unknown 7877578874 /estimated_length=unknown 8798087897.

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Submitted (12-NOV-1997) Molecular Biology, University of Nijmegen,
Submitted (1. Nijmegen 6525 ED, The Netherlands
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Location/Qualifiers
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Dechering, K.J., Kaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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CCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTATTTCTCTAGATTAGTAAAAAGGGA
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                                                                                              CTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAATGTT
                                                                                                                                                                    TAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTTAAGAGCTAG
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                                             TTTTTTTTTTTTTTTAATTTGAAATÄTÄTTTÄTTTATTTTCTACATÄTATAÄTÄÄTÄÄTÄ
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llarity 45.8%;
Conservative
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537. .>713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-JAN-1997) Department of Biology, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escalante, R., Wessels, D., Soll, D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on migA, a BTB protein Mol. Biol. Cell 8 (9),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 3576)

Escalante,R., Wessels,D., Soll,D.R. and Loomis,W.F.

Chemotaxis to CAMP and slug migration in Dictyostelium both depend
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                                                                                                                                            951. .1289
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/note="encodes |
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/notes"N-terminus of this protein is similar to other BTB
domain proteins, such as the Mus musculus and human zinc
finger proteins encoded by GenBank Accession Numbers
U14556 and L16896, respectively"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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chromosome="4"
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                                                        gene="migA"
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BTB

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	TTTGATTTTTCAAAAAAAATTAGTTTATTTCTCTTTAT 871	Qy 832 Db 432
	TCAAAAATCITICTGATTTITTTAAGAGCTAGTTTGGCAACCCIGTITCTITCAAAGAAT 831 	Qy 772 Db 492
	TITTATAAAATGACTATAAAGTCATITTTATATAAGAGCACGCATGTCGTAGATTCTCGT 771	Qy 712 Db 552
,	TATTITGITATIGITTITATATACATTITCTICTCTTACAATAGAGTGATITTCTTCCGA 711 	Qy 652 Db 612
•	AGCGACAAATTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTCATTCTTGT 651	Qy 592 рь 672
	CTTAAAAACAAGCATATTTCGAAAGAGACAATTATGTTACAGTTTACAAACATCTAAG 591 	Qy 532 Db 732
	TAATCCACTCGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCT 531	Qy 472 Db 792
	TGTCTAGTGTGCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAAC 471	Qy 412 Db 852
	1 5.4%; Score 71.2; DB 2; Length 3576; Similarity 47.2%; Pred. No. 0.0049; 17; Conservative 0; Mismatches 243; Indels 0; Gaps 0;	Query Match Best Local Sin Matches 217;
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ch completed: March 5, 2006, 21:55:43

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33

Title: Perfect score:

US-10-713-381-2\_COPY\_1\_1311 1311

1 ccatggtgtctctatgaaaa.....cgcacatatgtttcctgaac 1311

Sequence: Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0.

Minimum DB Maximum DB

seq length:
seq length:

2000000000

Total number of hits satisfying chosen parameters:

9993994

4996997 seqs, 3332346308 residues

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database

N\_Geneseq\_21:\*
1: geneseqn1980s:\*
2: geneseqn1990s:\*
3: geneseqn2000s:\*.

geneseqn2003bs:\*
geneseqn2003cs:\*

geneseqn2003ds:\*
geneseqn2004as:\*
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8

nucleic -

nucleic search, using sw model

Copyright

GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration

14.

March 5, 2006, 17:08:23; Search time 872.437 Seconds (Without alignments)
10014.946 Million cell updates/sec

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Adx4856 Bovine ES

Api61371 Soybean 2

Aai61372 Soybean 2

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Aai61373 Soybean 2

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Aai61374 Human imm

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Result No.

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Query Match
Best Local Similarity
Matches 1311; Conserv

100.0%; Score 1311; DB 2; 100.0%; Pred. No. 1.2e-269;

mismatches

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Sequence 1394

BP; 411

A; 309

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232

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0 Other;

Length 1394; Indels

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Gaps

TIC TO TO TO TURBUTUO COMPANDA INTO COMPANDA	961 GCCAGCCCATAAATIVATITAAACCGAAAACIGAAATCGAGCAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAA	GCCAGGCCCATAAATTATTTAAACCGAAACTGAAATGGAGCGAAACCAAATCTGAGCTAT		841 TTCAAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT 900 	781 TTTCTGATTTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTC	721 ATGACTATAAAGTCATTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC 780	661 ATTGTTTTATATACATTTTCTTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA 720	601 TTATATCGAAAGGTAAGACTTCAGATTTTTCTTTTCATTCTTGTTATTTTGTT 660			481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA 540	421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACT 480		THATTATTCTTEACATATTATTTAATTTTGGAAAAATAACAAACTATGCTTTGTGTA		181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240	CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT	AAAACTTCCACGGGTGCATGAT 120	1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60
Oy 61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	Qy 1 CCATGGTGTCTCTATGAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	Query Match 100.0%; Score 1311; DB 5; Length 1394; Best Local Similarity 100.0%; Pred. No. 1.2e-269; Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U;				XX  PT A male tissue-preferred regulatory region comprising nucleotide sequences  PT essential for initiating transcription of the MS45 gene useful for  PT mediating fertility in a male plant.	PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL; XX DR WPI; 2001-514772/56.	(PION-) PIONE	XX XX PR 15-FEB-2000; 2000US-00504487.	23-AUG-2001.	AA OS Zea mays. XX PN WO200160997-A2.	Ms45; male tissue; regulato hybrid seed; ds.	AC AAH/6332;  XX  DT 29-OCT-2001 (first entry)  XX  XX  XX  DF 7 mays Mad5 male tissue-preferred regulatory region encoding DNA.	RESULT 3 AAH76332 ID AAH76332 standard, DNA, 1394 BP. XX ANTON	1261 CCATCTTACTCATGCAAC	OY 1201 TTGTTCCATCGTCCAAGCCTTGCCTAATCCAAGCAAGAGATACCTACTCCCAAACAAT 1280 Db 1201 TTGTTCCATCGTCCAAGCCTTTGCCTATTCTGAACCAAGAGATACCTACTCCCAAACAAT 1280 Db 1201 TTGTTCCATCGTCCAAGCCTTTGCCTATTCTGAACCAAGAGGATACCTACTCCCCAAACAAT 1280 OY 1261 CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311	Oy 1141 GGTTCGGCAGCTCTCGTGT Db 1141 GGTTCGGCAGCTCTCGTGT	TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA

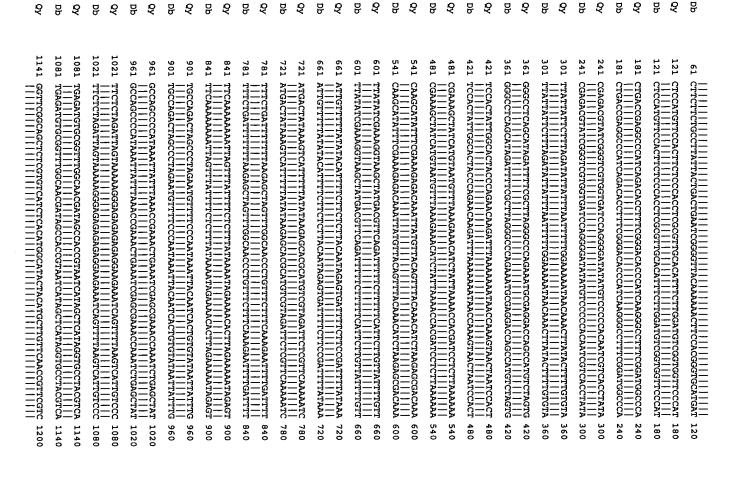
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                                                                                                                                            Query Match
Best Local Similarity
Matches 1311; Conserv
                                                                                                                                                                                                                                  The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 materials and the presents and the producing hybrid sequence encoding and ms45 materials.
                                                                                                                                                                                                                                                                                                                                                                                  A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z. mays Ms45 male tissue-preferred regulatory region encoding
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                                                                                                                                                                                              Sequence 1394 BP; 411 A; 309 C; 232 G; 442
                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 47; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-2000; 2000US-00504487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200160997-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hybrid seed; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ms45; male tissue; regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                          tissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mays
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                                                                                                        CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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CTCCATGTTCCACCTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTTCGGTGGTTCCCAT 180
                                                                                          CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
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                                                                                                                                             100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garnaat CW,
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                                                                                                                                            Score 1311; DB 5;
Pred. No. 1.2e-269;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huffman
                                                                                                                                                                                                                                                                                                                                                                                                comprising nucleotide sequences the MS45 gene useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kendall
                                                                                                                                              Indels
                                                                                                                                                                      Length
                                                                                                                                                                                                   0 Other;
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	1201 TIGTICCATCGTCCAAGCCTIGCCTATICTGAACCAAGAGGATACCTACTCCCAAACAAT 1260 	1141 GGTTCGGCAGCTCTCGTGTCATCACATGCATACTACATGCTTGTTCAACCGTTCGTC 1200	1081 TGAGATGTGCGGTTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA 1140 1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC 1200	TGAGATGTGCGGTTTTGGCAACGATAGCCACGTAATCATAGCTCATAGGTGCCTACGTCA	1021 TTCTCTRGATTAAAAAGGGAGAGAGAGAAGAAAATCAGTTTTAAGTCATTGTCCC 1080	961 GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020 	901 TGCCAGACTRACCCTAGAATGTTTTCCCCAATAAATTACAATGACTGTGTATAATTATTTG 960 901 TGCCAGACTAGGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTTTTTT		781 TTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTC	721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC 700	ATTGTTTTATATACATTTCTTCTCTTACAATAGAGGATTTICTTCGATTTATATAAAAATAGAGGATTTTCTTCTCTTACAATAGAGGATTTCTTCTCCGATTTTATATAAAATTTCTTCTTTACAATAGAGTGATTTCTTCCGATTTTATAAA	TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT	TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT	541 CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAA 500 [	CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAAA	481 CGARAGCTATCATGTAATGTTTAAAGARACATCTATTAAAACCACGATCCTCTTAAAAAA 540		GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCC	361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAAATGCGAGGACCAGCCAG	301 TTATTATTCTTTAGATATTTAATTTTTGGAAAAATAACAAACTTATACTTTTGTGTA 360		CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCCTTTCGGATGGCCCA 240	181 CTGANCGCTCCATCAGACACCTTTTCCGGACACCTTCCAACGCCCTTTCCGGATGGCCCA 240
-					-																\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.	**.	<del></del> ,
AC	X U A	RESULT	용 성	В .	\$ B	Qy Ma	ng Du Dis	ያ ያ ያ ያ ያ	ឧឧឧឧ	3 X X	1999X	<b>F</b>	# X	P X R	X P X	8 X	P X S	XXX	X II X	12 X	AAH763 ID A XX AC A	, Db	· Q
AGH /6334;	AAH76334 ID AAH76334 standard; DNA; 158 BP. XX	ILT 6	1265 CTTACTCATGCAACTTCCATGCAAACAGCACATATGTTTCCTGAAC 171	TCCATCGTCCAAGCCTTGC	5 ccdcdaarcccdrigrcaarccaaracaaracaaracaaracaaracaarccaaacaarccaar 1264 1205 TCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGCAGTACCTACTCCCAAACAATCCAT 1264	Matches 163; Conservative 0; Mismatches 4; Lineis v; vaps v; 1145 CGGCAGCTCTCGTGTCATCTCACATGCTACATGCTTGTTCAACCGTTCGTCTTGT 1204	ence 255 br; 55 A; 66 C; 55 G; 74 1; 6 0; 6 0000000;  atch 12.3%; Score 160.6; DB 5; Length 255;  cal Similarity 97.6%; Pred. No. 1.5e-24;	male fertility of the plant and (1) coming gene. A method of producing hybrid see sequence represents a Z. mays M845 promoted to the company of the company	number essential for initiating transcriptions of mediating male fertility in a plant is throducing an expression vector comprising to (1) into a plant where the exogenous gets.	, 8, 50pp	A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.	WPI; 2001-514772/56.	Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;	15-FEB-2000; 2000US-00504487. (PION-) PIONEER HI-BRED INT INC.	13-FBB-2001; 2001WO-US004527	23-AUG-2001.	Zea mays. WO200160997-A2.	Ms45; male tissue; regulatory region; transcription; male fertility; hybrid seed; promoter; ds.	Z. mays Ms45 promoter fragment.	29-OCT-2001 (first entry)	6340 AAH76340 standard; DNA; 255 BP. AAH76340;		CCATCTTACTCATGCAACT

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Best Local S
Matches 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -38 to -195 bases upstream of the TATA box of a Z. mays MS45 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ms45; male tissue; regulatory region; transcription; male fertility; hybrid seed; ds.
plant protectant; plant growth regulant; gene therapy; plant;
recombinant DNA construct; physical array; plant breeding marker;
cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-2001
                                                    Plant full length insert polynucleotide seqid 23340.
                                                                                 21-APR-2005
                                                                                                            ADX48600;
                                                                                                                                     ADX48600
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 47; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PION-) PIONEER HI-BRED INT INC
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157; Conserv
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                                                                                                                                                                                                                     GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
                                                                                                                                                                                                                                                                          CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                    CGTGTCATCTCACATGCCATACTACATGCTTGTTCAACCGTTCGTC-TTGTTCCATCGTC
                                                                                                                                                                                                      GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
                                                                                                                                                                                                                                                         CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
                                                                                                                                                                                                                                                                                                           CGTGTCATCTCACATGCATACATGCTTGTTCAACCGTTCGTCTTTGTTCCATCGTC
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nilarity 99.4%;
Conservative
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                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fox TW,
                                                                                                                                                                                                                                                                                                                                                                                                                   41 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue-preferred
                                                                                                                                      CDNA;
                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    50 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garnaat
                                                                                                                                      320
                                                                                                                                                                                                                                                                                                                                                                 <u>.</u>
                                                                                                                                                                                                                                                                                                                                                              Score 146; DB 5;
Pred. No. 1.7e-21;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                    21 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                    46 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huffman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising nucleotide sequences the MS45 gene useful for
                                                                                                                                                                                                                                                                                                                                                                                                                    U; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                    Other;
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                                                                                                                                                             Matches
                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LIUJ/)
(ZHOU/)
(KOVA/)
(SCRE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                      Sequence 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-180133/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-2003; 2003US-00425114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004034888-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .mproving yield.
       911
                                                                                                                                 791
                                                                                                   62
                                                                                                                                                             95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOVALIC D K.
SCREEN S E.
TABASKA J E.
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                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAO Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO
                                                                                                                        TTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTTGATTTTTTCAAAAAAA
       GCCCTAGAAT 920
                                       ATTAGTTTATTTTTCTTTGAGAAATAGAATTCCCTTGGGAAATTAGAGTTTCTAAACGA
                                                            ATTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTAGAAAAATAGAGTTGCCAGACTA 910
                                                                                                   TTTTTAGGGCTAGTTTGGAAATCTCATTTTTTCAAGAGATTTTTATTTTCCTAAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 J.
                                                                                                                                                                                                                      B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23340;
                                                                                                                                                                                                                      A; 53
                                                                                                                                                                          5.6%;
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                                                                                                                                                             0
                                                                                                                                                             Score 74; DB
Pred. No. 4.6e
0; Mismatches
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                                                                                                                                                                                                                        112
                                                                                                                                                             4.6e-06;
ches 35;
                                                                                                                                                                                                                      T; 0 U;
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                                                                                                                                                                                                                        0 Other
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182

GCCCTTAATT 191

ADX33444

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ADX33444 standard;

CDNA;

624

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The invention describes a recombinant DNA construct comprising a CC polynucleotide consisting of a sequence encoding an amino acid sequence CC available in electronic form from the US patent office at CC ftp.seqdata.uspto.gov/sequence.html?DooID:3004034888. The polynucleotide CC improving markers. The recombinant DNA construct is useful for plant breeding markers. The recombinant DNA construct is useful for cosmotic conditions, pathogens or pests, for manipulating growth rate in CC improving plant tolerance to cold, heat, drought, herbicides, extreme CC osmotic conditions, pathogens or pests, for manipulating growth rate in CC plant cells by modification of the cell cycle pathway, for conferring CC increased resistance to plant disease, for producing galactomannan, CC lignin or plant growth regulators, for increasing the rate of homologous CC recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake CC or by providing improved plant growth and development under at least one Stress condition or for modifying seed oil or protein yield and/or CC content. This sequence represents a plant full length insert CC invention of the used in the recombinant DNA construct of the
Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant protectant; plant growth regulant; gene therapy, plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; has tolerance; drought tolerance; hesticide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lighin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
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05-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 16264; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-180133/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein content; gene;
                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      improving yield.
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KOVALIC D K.
SCREEN S E.
TABASKA J E.
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                      Similarity
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  Conservative
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2001US-00985678.
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                                                                        BP;
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                                                                        170
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                  5.6%;
73.1%;
                                                                      A; 119
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    0;
                                                                      C; 146 G; 189 T; 0 U; 0 Other;
      Score 74; DB 13;
Pred. No. 5.4e-06;
0; Mismatches 35
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                                      Length 624;
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        Indels
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      밁
The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the segdata uspto gov/sequence.html?DocID:200403488. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; reduced tolerance; has tolerance; drought tolerance; hesticide tolerance extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                       New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
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05-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                               Claim 1; SEQ ID NO 32493; 15pp; English.
                                                                                                                                                                                                                                                                                                                                 Liu J,
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KOVALIC D K.

SCREEN S E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 content; gene;
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2001US-00985678.
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                                                                                                                                                                                                                                                                                                                                   Kovalic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA; 2445
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RESULT 10
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ID ADX34496/c
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Best Local S
Matches 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactcomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2445 BP;
  Claim 1; SEQ ID NO 17816; 15pp; English
                                                                             cold, heat,
pests, for o
                                                                                                                                                                                      WPI; 2004-180133/17
                                                                                                                                                                                                                                                                                                                                                                         (ZHOU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-1999;
05-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-APR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified.
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                                                    improving yield
                                                                          recombinant DNA construct, useful for improving plant tolerance to d, heat, drought, herbicides, extreme osmotic conditions, pathogens or to, for conferring increased resistance to plant disease, or for
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                                                                                                                                                                                                                                                                                                                    KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                    LIU J.
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                                                                                                                                                                                                                                                                                              CAO Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTAGTTCATTTTTCCTTGAGAAAATAGGAATCCCTTAAAAAAATAGTGTTTTCAAACTA 1742
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2001US-00985678.
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                                                                                                                                                                                                                                          Kovalic
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73.6%;
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Pred. No. 1
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ев 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                   extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                       plant protectant; plant growth regulant; gene therapy; plant;
recombinant DNA construct; physical array; plant breeding marker;
cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
(LIUJ/)
(ZHOU/)
(KOVA/)
(SCRE/)
                                                                                      06-MAY-1999;
05-NOV-2001;
                                                                                                                                                                                                             US2004034888-A1
                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                   protein
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                                                                                                                                       28-APR-2003; 2003US-00425114.
                                                                                                                                                                            19-FEB-2004
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n content; gene; ss.
                ZHOU Y.
KOVALIC D
                                                     LIU J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTTAAGAGCTGGTTTGGCAA-CCTCATTTTTCTAAGGGATTTCTATTTTACTAAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry
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                                                                                        2001US-00985678
                                                                                                      99US-00304517
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78.0%;
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Pred. No. 1.8e-
0; Mismatches
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L.8e-05;
hes 27;
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ADX 602:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a recombinant DNA construct comprising polynucleotide consisting of a sequence encoding an amino acid available in electronic form from the US patent office at ttp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynof the invention are also useful in physical arrays of molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides; extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for improving yield.
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(CAOY/)
                                                                                                        plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; harbicide tolerance; cold tolerance; harbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lighin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADX60218 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                 Plant full length insert polynucleotide seqid 31061.
                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTTAATGTTTTTTTTCATGAA 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTAGAATGTTTTCCCAATAAA 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAGTTCATTTTTCCTTGAGAAATAGGAATCCCTTAAAAAATAGTGTTTTCAAACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAGTTTATTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTAGGGCTAGTTTGAGAACCCT-TTTTTCCCAAAAGATTTTCATTTTTCAAAGAAAAA 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kovalic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA; 3607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.5%;
73.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 484~C; 524 G; 844 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DK, 'Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2.20
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 71.8;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   physical arrays of molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polynucleotide molecules and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
1 sequence
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Unidentified. protein

RESULT 13
AAL15210/c
ID AAL152
XX
AC AAL152
XX
DT 07-DEC
XX

AAL15210 AAL15210;

standard;

CDNA; 883

ВP

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07-DEC-2001

(first entry

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                                                                                                                                                                                                                                                                                                                        cc ftp.segdata.uspto.gov/sequence.html?poclip.2004034888. The polynucleotide cc of the invention are also useful in physical arrays of molecules and as cc improving plant tolerance to cold, heat, drought, herbicides, extreme cc osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring cc increased resistance to plant disease, for groducing galactomannan, cc lignin or plant growth regulators, for increasing the rate of homologous crecombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake cor by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert content. This sequence represents a plant full length insert content.
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                        Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the polymucleotide ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888, The polymucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2004034888-A1
                                                                                                                                                                                                                                                                           Sequence 3607 BP; 915 A; 695 C; 718 G; 1279 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 31061; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KOVA/)
                                                                 2930
2990
                                                                                                                                      2871 TCTTAGGGCTAGTTTGAGAACCCT-TTTTTCCCAAAAGATTTTCATTTTTCAAAGAAAAA
                              912
                                                                                                    852
                                                                                                                                                                       792 TITAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTCAAAAAAA 851
                                                                                                                                                                                                            105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZHOU Y.

KOVALIC D K.

SCREEN S E.

TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhou Y, Kovalic
                                                                                                                                                                                                                            Similarity
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                    CCCTAGAATGTTTTCCCAATAAA
                                                                                            TTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAG 911
CCCTTAATGTTTTTTTTCATGAA 3012
                                                                   Conservative
                                                                                                                                                                                                                        5.5%;
73.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DK,
                                                                                                                                                                                                            0
                                                                                                                                                                                                            Pred. No. 2.4e
0; Mismatches
                                                                                                                                                                                                                            Score 71.8;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screen
                                934
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                                                                                                                                                                                                            2.4e-05;
nes 37;
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                                                                                                                                                                                                                                               DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JE,
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                             Length 3607;
                                                                                                                                                                                                            1;
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Human breast

cancer expressed

polynucleotide

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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 237
                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human breast cancer expressed polynucleotides (AALD67544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JAN-2000;
14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 1378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUL-2000;
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09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JAN-2001;
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                                                                                                                                                                                599
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513
                         779
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                                                                                                      633
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                                                                                                                                                                                                                                                                                                                                            419 TGTCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCA
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                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                 AACAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACA
AAAAAAATTTTTTNAAANTNTTTTTAAAACCTTNAATTNAAANANAATTTTTTTNNNTT
                        TCTTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTGATT
                                                                                                                       TTATTGTTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATA
                                                                                                                                                        AATAANTTNAATTTTTTTAATNAAAAAAAAAATTTNAAATTTTAANCAANTNTTTTTT
                                                                                                                                                                           AATTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTTCTTTTTCATTCTTGTTATTTTG
                                                                                                                                                                                                            TTAAANNTTTTNTAANTTATTÄAACCAAAATTTTTTTTTAAAAAAATTTTTTAAAANTT
                                                                                                                                                                                                                                                              TANAAATTTTTTNAAAAACTAATTNTAANNATANTNAATTTTTNTAAAAAAANNNAAAAA
                                                                                                                                                                                                                                                                                       CTCGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAA
                                                                                                                                                                                                                                                                                                                  TGTTNANNNANACCTANACCTTTAAANATNTNNNANTTNAANNAAAAAATATTTAAANN
                                                   AAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAA
                                                                                                      Xu Υ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0192099P.
2000US-0193480P.
2000US-0205230P.
2000US-0211315P.
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0176077P.
2000US-0189167P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-US000798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3695pp; English.
                                                                                                                                                                                                                                                                                                                                                                               5.4%;
39.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                     A; 18 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          marker;
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                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                 Score 70.2; DB 4;
Pred. No. 3.8e-05;
0; Mismatches 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                     23 G; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                     T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                    367;
                                                                                                                                                                                                                                                                                                                                                                                                                       124 Other;
                                                                                                                                                                                                                                                                                                                                                                                             Length 883;
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                                                                                                                                                                                                                                                                                                                   814
454
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Query Match Best Local : Matches

Similarity

39.24;

0,

Score 70.2; DB 11; Pred. No. 3.9e-05; 0; Mismatches 367;

Indels Length

0,

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RESULT 14
ACN85231/c
ID ACN852
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                   The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003099974-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACN85231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN85231
Sequence
                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                               Novel isolated polypeptide associated with breast cancer, detecting presence of polypeptide in sample, as a marker:
                                                                                                                                                                                                                                                                                                                   Lillie J,
                                                                                                                                                                                                                                                                                                                                                                        18-JUL-2001; 2001US-0306220P
                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Breast cancer related marker,
                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2002; 2002US-00198846
                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1019
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flowering locus T gene; FT; terminal flower; TFL; Apetala3; Ap3; plant; floral development; plant sterility; plant fertility; flowering time; plant growth rate; inflorescence architecture; tissue culture morphology; cell division; FT homologue; gene; ds.
Danilevskaya O, Hermon P, Bruggemann E, Shirbroun D, Ananiev
Rafalski JA, Sakai H, 'Cahoon E, Cahoon R, Klein T;
                                                                                                                                                  30-JAN-2003; 2003US-00343477
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WPI; 2004-580996/56.
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New polynucleotides, specifically nucleic acid fragments encoding flowering locus T gene (FT) or terminal flower (TFL), or Apetala3 (Ap3) homologs, useful for floral development, e.g. engineering plant flowering time.

Claim 6; SEQ ID NO 63; 109pp; English.

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Crist, second, third, fourth or fifth nucleotide sequence, or their complement encoding a polypeptide either having flowering locus T gene (FT), terminal flower (TFL), or Apetala3 (Ap3) homologue activity. Also Creation of the comprising the polynucleotide; (2) a recombinant DNA construct comprising the polynucleotide; (3) a recombinant CR DNA construct comprising the polynucleotide; (4) a cell comprising the creating plant comprising the construct; (5) producing a plant comprising transforming call with the polynucleotide, and regenerating a plant from the construct; (7) a seed comprising the recombinant DNA construct; (8) an creating plant comprising the recombinant DNA construct; (8) an creating plant comprising a first nucleotide sequence contains at least 30 nucleotides, and where the creating plant producing a plant from the creating plant producing a plant from the creating plant producing and plant from the creating plant producing and plant from the creating plant producing and the polynucleotide comprising the polynucleotide where the creating plant polynucleotide includes the second, third, fourth, fifth or creating plant polynucleotide comprising isolating the polynucleotide comprising isolating the polynucleotide comprising isolating the polynucleotide comprising transformation. The present sequence represents an FT homologue nucleotide sequence from the present invention.

Sequence 13400 BP; 3962 A; 2948 C; 2695 G; 3795 T; 0 U; 0 Other;

S 밁 Ś 밁 á Matches 89; Query Match Best Local 8619 AAAAATAAAAATCCATTAGAAAAATGGGGTTGTCAAACTAGTCCTTATTTAGTTTTCCAT 8678 8559 ACCATTTTATTTTCAAGAGGTTTTTTATTTTATCAAGAAAATTAGTTCATTTTCTCTTTGG 8618 931 T 931 871 TAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCTAGAATGTTTTCCCAA 930 Similarity Conservative 5.3%; 73.6%; 0; Mismatches Score 69.8; DB 13; Pred. No. 9e-05; 32; Indels Length 13400; 0 Gaps

Search completed: March Job time: 873.437 secs 5, 2006, 18:11:41 밁

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# GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

t score:	Title: US-10	Run on: March	
1311 1 ccatggtgtctctatgaaaacgcacatatgtttcctgaac 1311	US-10-713-381-2 COPY 1 1311	March 5, 2006, 18:11:59; Search time 6189.32 Seconds (without alignments) 9910.279 Million cell updates/sec	

	Scoring table:
Gapop 10.0 , Gapext 1.0	IDENTITY_NUC

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : EST: \*
1: 9b
2: 9b
3: 9b gb\_est1:\*
gb\_est2:\*
gb\_est3:\*
gb\_htc:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb\_gss1:\* gb\_gss2:\* gb\_gss3:\*

### SUMMARIES

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o	6.4	6.4	6.5	6.5	6.5	6.5	6.5	6.5	. 6.5	6.6	6.6	6.6	6.6	6.7	6.7	6.9	7.0	7.3	32.0	51.8	69.3	Match	Query
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COSCILLATED	CL997678 ZMMBHt001	BZ816381 PUFBA86TD	AL175696 Tetraodon	CC433618 PUHHP17TD	CC630210 OGUCG53TH	CG349565 OG0FI83TH	CC630219 OGUCG53TV	CG082135 PUFQX12TD	CG103452 PUJBE19TB	CC400574 PUHLU61TB				N	CG048704 PUILO19TB	CZ295176 ZMMBF0063	CL235046 ZMMBBb057	CG252571 OG4BB05TC	CC656939 OGWDQ20TV	CG224225 OG1AG08TV	CC656933 OGWDQ20TM	Description	

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CC385762 PUHFK14TD CG221693 OGMMG04TF AL078714 Drossophil DR794756 ZM BEPD011 EZ996930 PUGIRSOTB CC676387 OGKAS81TH CG246849 OGWAL22TF		CG034985 PUIGRERETE BE797976 PUIGREPSTE BC430754 PUHEPOSTE CG102092 PUFYW94TE CC435780 PUHSW02TD BZ784278 PUFHV09TD CC620594 OGUCCZ6TV	CG333914 OG0AD14TF
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# ALIGNMENTS

404 ACCAGCCATGTCTAGTGTCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACC 463	δ
tch 69.3%; Score 908; DB 9; Length 963; al Similarity 100.0%; Pred. No. 9.6e-180; 908; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Best Local Matches 90
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/clone="ZMMBMa0554D15"	
/strain="B73" /dh wref="tayon:4577"	
/mol_type="genomic DNA"	•
/organism="Zea mays"	Bource
	FEATURES
Class: methylation filtered.	
Seq primer: TR	
Email: whitelaw@tigr.org	
Fig. 101 - 838-0208	
9712 Medical Center Drive, ROCKVIIIe, ND 20030, 035	
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Contact: Cathy Whitelaw	
Other GSSs: OGWDQ20TV	COMMENT
Unpublished (2002)	JOURNAL
	TITLE
kenbush, J., Van Aker	AUTHORS
	REFERENCE
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAU	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	ORGANISM
Zea mays	SOURCE
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Class: methylation filtered.
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback, Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback, Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rccitek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: GG1AG08TH
Contact: Cathy Whitelaw
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Fax: 301-838-0208
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/mol type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMa0716B15"
/clone=lib="ZM_0.7.1.5_KB"
/note="Vector: pBcSK-; Site_1: H:methylation filtered genomic DNA
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1 (Dases I to 687)

1 (Dases I to 687)

Richick, A., Guackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: GCMDQ20TM

Contact: Cathy Whitelaw
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelnw@tigr.org
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methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                             195 TCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCACGAGACGTATCGGG
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Zea mays
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pac
clade; Panicoideae; Andropogoneae; Zea
(1) (bases 1 to 715)
(clade, R. W., Quackenbush, J., Van Aken, S., Utterback, T.,
Rhitelaw, C.A., Praser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG252571
715 bp DNA linear GSS 25-AUG-2003
CG4BB05FC ZM 0.7_1.5 KB Zea mays genomic clone ZMMBMa0809B10,
genomic survey sequence.
CG252571
CG252571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive, Rockville, MD 20850,
Tel: 301-838-5843
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 7.3%;
Similarity 80.1%;
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       smail: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/mol type="genomic DNA"
/strain="B73"
/strain="B73"
/db xref="reaxon:4577"
/clone="ZMMBMA0809B10"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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Pred. No. 1.5e-09;
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CZ295176
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Best Local Similarity 78.6%;
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ZMMBF0063M20f ZMMBF 2

Burvey sequence.

CZ295176
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Seq primer: SP6
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Tel: 732 445 3801
Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bro Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing, Sequencing of the maize genome at PGIR (2003c)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 967)
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ZMMBBb0575001r
                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                               1 (bases 1 to 860)
Bharti, A.K., Nelson
                                                                                                              Zea mays
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Construction,
                and Messing, J.
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Location/Qualifiers
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/cultivar="B73"
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/clone_lib="ZMMBBb (HindIII)"
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clone="ZMMBBb0575001"
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                               Nelson, A.B.,
 Sequencing and
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Pred. No. 1e-08;
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                               Young, S.,
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                               Keizer, G.,
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ing, J.
   of a
                               Zohovetz, V.,
   Fosmid Library
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aceae; PACCAD
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Tel: 732 445 3801
Fax: 732 445 5735
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Unpublished (2005)
Contact: Bharti, A.K.
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The Plant Genome Initiative
                            9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                    Maize Genomics Consortium Unpublished (2003) Other GSSs: PUILO19TD Contact: Cathy Whitelaw
                                                                                                                                                                     Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 814)

1 (bases 1 to 814)

1 (bases 1 to 814)

1 (bases 1 to 814)
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PUILO19TB ZM_0.6_1.0_KB
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               Email: whitelaw@tigr.org
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Seq primer: TR
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/cultivar="B73"
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clone_lib="ZMMBF"
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                                                                                                                                                            Fraser, C.M.,
                                                                                                                                                                                                                                                                                           GI:33920884
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Pred. No.
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1.7e-08;
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genomic
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l,P., Ma,J. an
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CG414922/c
                                             FEATURES
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Best Local
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence. CG414922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CG414922 754 bp DNA lir
ZMMBBb0290L09.r ZMMBBb Zea mays genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                          clade; Panicoideae; Andropogoneae;
1 (bases 1 to 754)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG414922.1 GI:34505144
                                                                                                                                                                                                                 Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A,
                                                                                                                                                                                                                                                             Sequencing of the maize genome Unpublished (2003) Contact: Rod Wing
                                                             Plate: 0290 row
Seq primer: M13r
Class: BAC ends.
                                                                                                            BACKWARD:
                                                                                                                                                                  Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                               and Wing, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTT 772
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                                                                                                                                         PRimers
                                                                                                                                                                                                                                                                                                                              Kim, H.R., Hatfield, J., Soderlund, C.,
                                                                                                                                                       rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="ZMMBTa0611C13"
/clone lib="ZM 0.6 1.0 KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:4577"
                                                                                                          M13r
/organism="Zea mays"
/mol_type="genomic DNA"
                                           Location/Qualifiers
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                                                                                              row: L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 88; DB 10;
Pred. No. 7.1e-08;
                                                                                              column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                              9
                                                                                                                                                                                                                        P.O. Box 210088, Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear GSS 08-SEP-2003 one ZMMBBb0290L09 3',
                                                                                                                                                                                                                                                                                                                                 Bharti, A.K., Messing, J
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CC439901/c
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Best Local S
Matches 126
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            241
                                         787
                                                                          126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize Genomics Consortium Unpublished (2003) Other GSSs: PUHRV15TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases I to 950)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., San Wiguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays
Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                   Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                            Seq primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                         Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAAT 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTCAAAAAAAATTAGTTTAATTTTCTCTTTTATAAAATAGAAAACACTTAGAAAAAATAGA 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
            ATCTTTCTAATGACTAGTTTGGGAACCTTATTT-TCTCACGGGATTTTTTATTTTTCAAT 183
                                  ATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTCAAA 846
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/db_xref="taxon:4577"
/clone="ZMMBBb0290L09"
                                                                                                                                                  /clone="ZMMBTa519D06"
/clone lib="ZM_0.61.0 KB"
/clone lib="ZM_0.61.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
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                                                                                                                                                                                                                                              organism="Zea mays"
/mol_type="genomic DNA"
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                                                                        Score 86.8; DB 9; Length 950; Pred. No. 1.3e-07; O; Mismatches 47; Indels
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EcoRI; 0.6-1.0 kb

high

Gaps

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RESULT 11
CC400575/c
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                                                     521
                                                                              894
                                                                                                        461
                                                                                                                                 834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUHOC67TB ZM_0.6_1.0_KB genomic survey sequence. CC384247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropgoneae; Zea.

1. (bases 1 to 652)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: TR
Class: sheared ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Resnick, A., Fraser, C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whitelaw, C.A., Quackenbush, J.,
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                                                                                                                                                                                                                                       TTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTC
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                                                     ATTAGGTTTCCAAACTAGCCCTAAA 545
                                                                           ATAGAGTTGCCAGACTAGCCCTAGA 918
                                                                                                       TGATTTTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAA
                                                                                                                                                             AGAATCTTATTTATTAATGTTAAGAGCTAGT
                                                                                                                                                                                     primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301-838-0208
                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                 /clone="ZMMBTa495L13"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                   organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                               6.6%;
                                                                                                                                                                                                                                                                Score 86.6; DB 9;
Pred. No. 1.4e-07;
0; Mismatches 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      652 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Aken,S., Utterback,T.,
Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic clone
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ZMMBTa495L13,
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PUHLUGITB ZM 0.6
genomic survey s
CC400574
CC400574.1 GI:3
GSS.
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1 (Dases 1 to 797)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC400575
CC400575.1 GI:30880665
GSS.
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PUHLU61TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa480L01,
Zea
Zea
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Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
Other_GSSs: PUHLU61TB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: whitelaw@tigr.org
Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize Genomics Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                     <u>AAATAGAGTTCTCAAACTAGCCCTAAGGTTATATCCGATAAATCCCCTATCTCATTCTCT</u>
mays
mays
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/clone="zMMBTa48DL01"
/clone=1ib="ZM_0.6 1.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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59.7%;
                                               GI:30880664
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Pred. No. 1.4e-07;
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                                                                                             mays
                                                                                          DNA linear GSS 19-MAY-2003 genomic clone ZMMBTa480L01,
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a; Poales; Poaceae; PACCAD
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  952 AATTATTIGGCCAGCCCCATAAATTATTTAAAC 984
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Zea mays
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 471)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 820)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                            CG103452 471 bp DNA linear GSS 20-AUG-2003
PUJBE19TB ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTa0628D13,
genomic survey sequence.
CG103452
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Class: sheared ends.
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Other_GSSs: PUHLU61TD
                                                                                                                                                                                                                      CG103452.1 GI:33985746
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/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0
CoT selected genomic DNA library"
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mol_type="genomic DNA"
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59.7%;
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Pred. No. 1.4e-07;
D; Mismatches 109;
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4e-07;
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AUTHORS
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CG082135/c
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Zea mays
                                                                                                                                                                                                                                                          Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFQX12TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CG082135 765 bp DNA linear GSS 20-AUG-2003 PUFQXI2TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0712B24, genomic survey sequence.
CG082135 CG082135 GI:33964429
                                                                                                                                                        9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Spermatophyta, Magnoliophyta, ililopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Other GSSs: PUJBE19TD
                                                                                                                     Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 765)
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/clone=lib="ZM 0.6_1.0_KB"
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CoT selected genomic DNA library"
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/strain="B73"
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/db_xref="taxon:4577"
                     organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                             Location/Qualifiers
                                                                                   . 765
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Pred. No. 2.4e-07;
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OGUCG53TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0406J09,
genomic survey sequence.
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1 (bases 1 to 781)

Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
Other_GSSs: OGUCG53TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cathy Whitelaw
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methylation_filtered_genomic_DNA_library"
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/mol_type="genomic DNA"
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and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                    ATTGTTTTTATATACATTTTCTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA
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TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAGAGAAATCAGTTTTAAGTCATTGTCCC
                                         GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT
                                                            GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT
                                                                                                 TGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTG
                                                                                                              TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTAGTTTG
                                                                                                                                                         TTCAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT
                                                                                                                                                                         TTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTAGAAAAAATAGAGT
                                                                                                                                                                                                                 TTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTGATTTT
                                                                                                                                                                                                                                 ATGACTATAAAGTCATTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC
                                                                                                                                                                                                                                                                                                                                ATTGTTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA
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; LENGTH: 1394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic US-08-880-499-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-08-880-499-2
; Sequence 2, Application
; Patent No. 6037523
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                                                                                                                                                                                                                                                NAME: Sweenby, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Box 1000
STREET: Box 1000
STRIET: Johnston
STATE: Iowa
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
CITY: 5011
                                                                   Query Match
Best Local Similarity
Matches 1311; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,499
FILLING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Albertson,
APPLICANT: Fox, Tim W.
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
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                     CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
                                                                                                                                                              DNA (genomic)
                                                                                        100.0%;
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                                                                       ٥,
                                                                       Score 1311; DB 3;
Pred. No. 8.7e-305;
, Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #
                                                                                                           Length
                                                                         Indels
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음 정

Db 5606	_	1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC 1200
. QY . 792		1081 TGAGATGTGCGGTATGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA 1140
Matches 93		1081 TGAGATGTGGGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA 1140
Query Mat		1021 IIC.ICIANAIIAN IANANAN SANANAN KANANAN KANANAN ININAN ININAN ININAN ININANAN ININANAN ININANAN ININANAN ININANAN ININANANAN ININANANANA
; LIBRARY ; CLONE: ; 08-968-542C		
, IMMEDIATE , LIBRARY		GCCAGCCCCATAATTATTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT
; ANTI-SENS ; ORIGINAL ; ORGANIS		901 TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTTG 960
TOPOLOG;  MOLECULE;  DESCRIP;  HYPOTHETI		841 TTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT 900. 
; SEQUENCE ; LENGTH: ; TYPE: ; STRANDE:	<del></del>	781 TITCTGATTITTTAAGAGCTAGTITGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTT 840 
; TELECOMMU ; TELEPHOI ; TELEPAX ; INFORMATION		721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC 780 
; ATTORNEY/I ; NAME: I ; REGISTRI ; REFERENO		661 AITGIITTIATAIACAITTICTTCICTIACAAIAGAGIGAITITICTICCGAITTIATAAA 720 
CLASSIFI PRIOR APPLICATION PILING I		601 TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT 660
SOFTWARE CURRENT AF APPLICAT FILING I		541 CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAA 600 
2999		481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA 540
CITY: ISTATE: COUNTRY: 7		421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACT 480
		361 GGGCCTCAGCATAGATITTCGCTTAGGGCCCAGAAATGCCGAGGACCAGCCATGTCTAGTG 420
E OF	<del></del>	301 TTATTATTCTTTAGATATTATTTAÄTTTTTGGAAAAATAACAAACTTATACTTTTGGTA 360 
RESULT 3 US-08-968-542C- ; Sequence 1, A ; Patent No. 59	-	241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA 300
		181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240
	·	121 CTCCATGITCCACTICTCCCACCTCGCGTTGCACATTICTTGGATGTCGGTGGTTCCCAT 180
Db 1141 G	\$	61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120

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AL SOURCE:
NISM: maize
JE TYPE: endosperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ER READABLE FORM:
UM TYPE: 3.5 floppy disk
UTER: Apple Macintosh
ATING SYSTEM: Macintosh
WARB: Microsoft Word 6.0.1 for Macintosh
T APPLICATION DATA:
IT APPLICATION NUMBER: US/08/968,542C
SIFICATION: 800
APPLICATION JATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           SY/AGENT INFORMATION:
Benjamin Aaron Adler, Ph.D., Grent Andrey, Ph.D., Grent NUMBER: 35,423
STRATION NUMBER: D6036
MUNICATION INFORMATION:
MUNICATION INFORMATION:
HONB: (713) 777-2321
                                                                                                                         RY: maize endosperm cDNA library in
RY: (gtl1
: pMgf10; pMg6Aa; pMgt6-2M
2C-1
                                                        h 5.1%; Score 66.4; DB 2; Similarity 77.5%; Pred. No. 5.2e-06; 93; Conservative 0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houston
TX
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T: Myers, et al.
INVENTION: dullI Codes For A No. 5981728el
INVENTION: Synthase
P SEQUENCES: 35
NDENCE ADDRESS: 35
SEE: McGregor & Adler, LLP
: 8011 Candle Lane
                                                                                                                                                                                                                                                                   PTION: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERISTICS:
: 6027 bp
nucleic acid
EDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08968542C 981728
TCTACGGGCTAGTTTGGGAACCCCATTT-TTCCAAGGGATTTCCATTTTTTCCAAGAAAAA 5548
                   : (713) 777-6908
FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                  linear
                                                                 Indels
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APPLICANT: Wyers, Alan M.

APPLICANT: Wyers, Martha G.

APPLICANT: James, Martha G.

FITTLE OF INVENTION: dull1 Coding for a No. 6639125el Starch Synthase and Uses

FILE OF INVENTION: Thereof

FILE REFERENCE: D6036PCT

CURRENT PILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: PCT/US98/24225

PRIOR APPLICATION NUMBER: PCT/US98/24225

PRIOR APPLICATION NUMBER: US 08/062,102

PRIOR APPLICATION NUMBER: US 08/062,102

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-12

FRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION MYMBER: US 08/062,102

PRIOR APPLICATION NUMBER: US 08/062,102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-09-554-467A-1/c
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US-08-410-784A-3/c
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OTHER INFORMATION: CDNA sequence corresponding to the gene encoding the
OTHER INFORMATION: starch synthase enzyme DU1.
US-09-554-467A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Applic
Patent No. 5912413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09554467A Patent No. 6639125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
              COMPUTER: IBM Compatible
OPERATING SYSTEM; DOS
SOFTWARE: FABLSEQ Version 1.5
SCURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,7
FILING DATE: 24-MAR-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MYERS, ALAN M.
APPLICANT: JAMES, MARTHA G.
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin and Hayes LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TITLE OF INVENTION:
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                  CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                              ZIP: 02109
                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 5.1%; ocal Similarity 77.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                852 TTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAAATAGAGTTGCCAGACTAG 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
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                                                                                                                                                                                                                                                                                                                                                                                             Ten Post Office Square
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                                                                              US/08/410,784A
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OF THE
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RESULT 6
US-08-487-826B-13/c
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Best Local Similarity
           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA: US/08/487,826B
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: chitnis, Chetan
APPLICANT: willer, Louis H.
APPLICANT: Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Peterson, David
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas
TITLE OF INVENTION: BINDIN
TITLE OF INVENTION: AND PI
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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NAME: Heine, Ph.D., Holliday C
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: ISU-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2523 base pair
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic
STRANDEDNESS:
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                                                                                                                                                                                                                                                         STREET: 620 Newport
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-451-0313
                                                                                                                                                                                                                                      COUNTRY:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                           Thomas E.
                                                                                       US/08/487,826B
29,655
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Pred. No. 0.00029;
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                                                                                                                               Version
                                                                                                                                                                                                                                                                                                  16th Floor
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RESULT 7
US-09-662-254B-26/c
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Best Local Similarity 50.2%;
Matches 141; Conservative
                                                                                                            Query Match
Best Local (
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                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1

SEQ ID NO 26

LENGTH: 50000

TYPE: DNA

ORGANISM: Amsacta moorei entomopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bawden, Alison Louise
TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologou
TITLE OF INVENTION: Vertebrate Cells
FILE REFERENCE: UF-221C1XC1
                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 80
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/2 PRIOR FILING DATE: 2000-08-10
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/662,254B CURRENT FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Moyer, ]
APPLICANT: Li, Yi
APPLICANT: Bawden
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LENGTH: 19124 base pai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL:
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                     27972 ÁTÁTGTATTAACCAATAAÁÁÁATTÁÁAAAATGAÁATCAAATTTATTACACCTAATAATAT 27913
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/086,651 FILING DATE: 1998-05-29
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                                                      315 ATATTATTTAATTTTTGGAAAAATAACAAACTTATACTTTTGTGTAGGGCCTCAGCATAG 374
                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTCAAAAAAATT 853
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                                                                                             <u>,</u>
                                                                                                            Score 56.4; DB 3;
Pred. No. 0.0026;
                                                                                             Mismatches
                                                                                             306;
                                                                                                                             Length 50000;
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                                                                                                                                                                                                         NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700350078H1
NAME/KEY: unsure
LOCATION: 10, 12, 185-186, 204, 253, 274, 278
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-5397
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US-09-313-294A-5397
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SOFTWARE: PEKE
SEQ ID NO 5397
SEQ TRNGTH: 279
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                                                                                                                                  Matches
                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lalgudi,
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27792 TAAATATACAAAATATAATTAATAATTACAATAATAATGTTAAAAAATAAAGAATTATTAAA 27733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             668 TTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTA 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 ATTITCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTGTCCACTATTGGCAC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    728 TAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGA 787
849 AAATTAGTTTATTTTCTCTTTAT-AAAATAGAAAACACTTAGAAAAAATAGAGTTGCCAGA
                                                                                               789 TTTTTTAAGAGCTAGTTTGGCAACCCCTGTTTCTTTCAAAGAATTTTTGATTTTTTCAAAAA 848
                                                                                                                                    89;
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                                                            TTCCTAANGNCCTAGTTTGGAAACCCCATTTTCCCCACGGGTTTTTCATTTTCCCAAGGG 62
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                                                                                                                                      Conservative
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                                                                                                                                                   4.3%;
                                                                                                                                  ; Score 55.8; DF; Pred. No. 0.000
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                                                                                                                                                     DB 3;
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                                                                                                                                                                           Length 279;
                                                                                                                                      Indels
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                                                                                                                                      Gaps ·
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
ITILE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1357
LENGTH: 612
TYPE: DNA
ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-09-902-540-1357/c
; Sequence 1357, Application US/09902540
; Patent No. 6833447
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; NAME/KEY: unsure
; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357
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                                                                                                                                                      Sequence 1, Application US/08880499
Patent No. 6037523
GEMERAL INFORMATION:
APPLICANT: Albertson, Marc C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                             APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
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                                                                                                                                                                                                                                                                                                                                   CTTTATA 872
                                                                                                                                                                                                                                                                                                  TATTTTA 314
                                                                                                                                                                                                                                                                                                                                                                      TGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTCAAAAAAATTAGTTTATTTTCT
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nilarity 51.4%;
Conservative
PIONEER HI-BRED INTERNATIONAL, INC
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Pred. No. 0.00094;
0; Mismatches 120; Indels
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RESULT 11
US-08-880-499-2/c
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                                                                                                                                                                                                                 APPLICANT: Albertson, Marc C.
APPLICANT: Albertson, Marc C.
APPLICANT: Fox, Tim W.
APPLICANT: Fox, Tim W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
APPLICANT: Kendall, Marc MTSGII
                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08880499 Patent No. 6037523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.2%;
Best Local Similarity 55.8%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,499
APPLICATION NUMBER: US/08/880,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248-4800
                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER H
                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O. STREET: Box 1000 CITY: Johnston
COUNTRY: US
ZIP: 50131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1394 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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                                                                              STREET: Darwin Bu
STREET: Box 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                            STATE:
                                                             CITY: Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           830 TYCTYTGAAAGAAACAGGGTTGCCAAACTAGCTCTTAAAAAAATCAGAAAGATTTTTGAA
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: Iowa
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                                      Iowa
                                                                                               E: PIONEER HI-BRED INTERNATIONAL, INC.
Darwin Building, 7100 N.W. 62nd Ave.,
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MALE TISSUE-PREFERRED REGULATORY REGION
AND METHOD OF USING SAME
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Pred. No. 0.0012;
0; Mismatches 84;
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N. C. Color

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; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1055
; OTHER INFORMATION: c
US-09-806-708B-23
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US-09-806-708B-23
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Best Local Similarity. 55.8%;
Matches. 106; Conservative
        Query Match
                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 23
SOFTMARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 1055
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Applica
Patent No. 6784342
GENERAL INFORMATION:
Query Match 4.2%; Score 55.4; DB 3; Length 1055; Best Local Similarity 22.5%; Pred. No. 0.0013; Matches 182; Conservative 181; Mismatches 430; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1394 base not tryon
                                                                                                                                                                                                                                                                                 APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 6/147,133
PRIOR PRIOR DATE: 1999-08-04
                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: C
CLASSIFICATION:
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DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACTGTGTA 950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAATGTTTTCCCCAATAAATTACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTCAAAGAATTTTGATTTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAA 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09806708B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1394 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                              consensus sequence of A.t. and L.a. FAE1 promoters
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; Pred. No. 0.00:
0; Mismatches
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      Indels 15;.
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SEQ ID

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NOS:

CURRENT APPLICATION NUMBER: US/09/004,056A CURRENT FILING DATE: 1998-01-07 EARLIER APPLICATION NUMBER: 6034914 EARLIER FILING DATE: 1997-07-01

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                                                                                                                                              RESULT 13
US-09-004-056-1/c
                                             APPLICANT: Calgene LLC
                                                                                           Sequence 1, Application US/09004056A Patent No. 6566586
TITLE OF INVENTION: Plant Expansin Promoter FILE REFERENCE: 125
                                                                                                                                                                                                                                                                                             1057 AAATCAGTTTTAAGTCATTGTCCCTGAG 1084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 TTTTGTGTAGGGCCTCAG-CATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCC 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 WYGASWAGNASTRRTTYTWRWKWMCKRKSARARATRGRARYMRAWYTAWARRTGWTKAMA
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                            Sequences
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US-09-640-173-53
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                                                                                                                                   US-09-640-173-53
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; SEQ ID NO 53
; LENGTH: 396
; TYPE: DNA
ORGANISM: Homo sapien
; FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 53, Application US/09640173
Patent No. 6613515
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Best Local :
                                                                              Query Match
Best Local Similarity
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                                                                  Matches
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APPLICANT: Stolk, John A.
TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 210121.484C2
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/640,173
CURRENT FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 196
SOFTWARE: FABESEQ for Windows Version 3.0
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LOCATION: (956)
OTHER INFORMATION: unknown nucleotide
                                                                                                                                             NAME/KEY: misc feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C
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NAME/KEY: promoter
LOCATION: (947)
OTHER INFORMATION: unknown
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LOCATION: (930)
OTHER INFORMATION: unknown nucleotide
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                      TITITCTTTTTCATTCTTGTTATTTGTTATTGTTATTATATACATTTTCTTCTCTTACA 691
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Pred. No. 0.0019;
0; Mismatches 128;
                                                               Score 55; DB 3; Length 396
Pred. No. 0.0011;
0; Mismatches 178; Indels
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Sequence 53, Application US/09713550

PAtent No. 6617109

GENERAL IMPORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVI

FILE REFERENCE: 210121.48424

CURRENT APPLICATION NUMBER: US/09/713,550

CURRENT ETLING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 205

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 53

LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or
US-09-713-550-53
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US-09-713-550-53
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Best Local Similarity 43.8%;
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IENGTH: 396
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191
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                                                                                                                                                                                                                                                                                               251
                                                                                                                                                         CGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTAAGAGCTAGTTTGGCAA
                                                                                                                  CCCTGTTTCCAAAGAATTTTGATTTTTTCAAAAAAAATTAGTTTATTTTCTCTTTAT 871
                                                                                                                                                                                                                   AAATTACAATCACTGTG
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       AAATTACAATCACTGTG
                                                                                              CGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTAAGAGCTAGTTTGGCAA 811
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                                                                AAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAATGTTTTCCCCAAT 931
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Search completed: March 5, 2006, 22:36:25 Job time : 367.534 secs THIS PAGE BLANK (USPTO)

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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/cgn2-6/ptodata/2/pubpna/USO9_NEW_PUB.seq: *
/cgn2-6/ptodata/2/pubpna/USO9_NEW_PUB.seq: *
/cgn2-6/ptodata/2/pubpna/US10_NEW_PUB.seq: *
/cgn2-6/ptodata/2/pubpna/US11_NEW_PUB.seq: *
/cgn2-6/ptodata/2/pubpna/US11_NEW_PUB.seq: *
/cgn2-6/ptodata/2/pubpna/US11_NEW_PUB.seq: *
/cgn2-6/ptodata/2/pubpna/US11_NEW_PUB.seq3: *
/cgn2-6/ptodata/2/pubpna/US11_NEW_PUB.seq4: *
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11 US-11-014-071-2

8 US-10-240-708-36

7 US-10-330-773-534

6 US-09-925-065A-84272

8 US-09-925-065A-803046

8 US-10-240-708-3

8 US-10-940-708-63

8 US-10-995-561-13314

6 US-09-925-065A-803045

17 US-10-340-708-1

17 US-11-330-773-242

18 US-10-925-065A-667263

19 US-10-93-925-065A-667263

10 US-09-925-065A-667263

10 US-09-925-065A-67263

10 US-09-925-065A-67263

10 US-09-925-065A-67263

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2 US-11-191-893-182

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3 6 US-09-925-065A-206148
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Sequence 34, Appl
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Sequence 54, Appl
Sequence 63, Appl
Sequence 73, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 66, Appl
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Sequence 77, Appl Sequence 91, Appl	Sequence 714059, Sequence 714060,	Sequence 35, Appl Sequence 963, App	Sequence 46, Appl Sequence 42, Appl Sequence 80, Appl	Sequence 3, Appli Sequence 3, Appli	Sequence 13, Appl Sequence 25, Appl	Sequence 835, Appl Sequence 835, App	Sequence 96, Appl Sequence 242, App	2061		Sequence 667264, Sequence 667266,

# ALIGNMENTS

Oy 730 AAGTCATTTTATATAAGAGCACGCATGTGGTAGATTCTCGTTCAAAAATCTTTCTGATT 789	Qy 670 ATATACATTITCTTTCTTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATA 729	Query Match 5.2%; Score 68; DB 11; Length 1092; Best Local Similarity 57.3%; Pred. No. 0.0063; Matches 142; Conservative 0; Mismatches 105; Indels 1; Gaps	; NAME/KEY: promoter ; LOCATION: (1)(1092) ; OTHER INFORMATION: P95 US-11-014-071-2	; LENGTH: 1092 ; TYPE: DNA ; ORGANISM: Zea mays ; PEATURE:	D 20	CURRENT FILING DATE: 2004-12-16  PRIOR APPLICATION NUMBER: 60/530,478  PRIOR FILING DATE: 2003-12-16  PRIOR APPLICATION NUMBER: 60/591,975  PRIOR APPLICATION NUMBER: 60/591,975	; APPLICANT: WIL YOUNG MINISTER SUPPRESSION Transgenes and TITLE OF INVENTION: Deminant Gene Suppression Transgenes and TITLE OF INVENTION: Methods of Using Same FILE REFERENCE: 1554 ; CURRENT APPLICATION NUMBER: US/11/014,071	9	RESULT 1 US-11-014-071-2 ; Sequence 2, Application US/11014071 ; Publication No. US20050246796A1 GRAFFANT INCOMMENTON:
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US-10-240-708-36
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CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR PPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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Publication No. US20050282157A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Dispnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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 TAAGATTTTATTTTGTT
                                   AAAATTAGTTTATTTT 863
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                                                                         ATTTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTGATTTTTCAAA
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Sequence 534, Application US/10330773

Publication No. US20060040262A1

GENERAL INFORMATION:

APPLICANT: David W. Morris

APPLICANT: Marc Malandro

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

FILE REFERENCE: 529452001300

CURRENT APPLICATION NUMBER: US/10/330,773

CURRENT APPLICATION NUMBER: US/20773

NUMBER OF SEQ ID NOS: 981

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 534

LENGTH: 254396
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US-10-330-773-534
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; ORGANISM: Homo sapiens
US-10-330-773-534
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
                                                                                                                                                                                                                                                                                                                                                                                                        US-09-925-065A-54272
                                                                                                                                                                                                                                                                 Sequence 54272, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTGTTTCTTCAAAGAATTTTGATTTTTCAAAAAA 849
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Pred. No. 3
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; ORGANISM: Homo sapiens
US-09-925-065A-54272
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US-09-925-065A-803046
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NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FactSEQ for Windows Version
SEQ ID NO 54272
LENGTH: 915
                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-925-065A-803046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.2%;
Best Local Similarity 51.0%;
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 803046, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                              Matches 137;
                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPILICANT: Wang, David G.
RITLE OF INVENTION: Identification and Mapping of Single
RITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                       ID NO 803046
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                                                  37
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                                                                                                                              Similarity
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                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            David G.
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                                                                                                                            4.1%;
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1; Mismatches
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Pred. No. 1
                                                                                                                1;
                                                                                                                                Score 53.6;
Pred. No. 1.
                                                                                                                 ed. No. 1.7;
Mismatches 140;
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                                                                                                                                                DB 6; Length 488;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/EP01/03971 PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/240,708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: DE 10043826.1
                                                       3897
                                                                                                                                                                                                                                                                                                                                        4137 СТАСАЛТСССААСТАСТСААААЛТСТСАААСААААААЛАТААСТТАААССССАААААТТСАА 4078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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                                                                                                                                                                                                                                                                    277 IGTTCTTTTTTTTTTTTTTAGAAAAAAAAACACTT 314
                                                                                          665
                                                                                                                                                            605 ATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTGTTATTG 664
                                                                                                                                                                                                                                 545 CATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGGGACAAATTAT 604
                                                                                                                                                                                                                                                                                                     485 AGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAG 544
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19; Conservative
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                                                     TTTTTATATACATTTT-CTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAAATG:723
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APPLICANT: OLEK, Alexander
APPLICANT: DIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE: 5013.1012
CURRENT SPELICATION UNMBER: US/10/240,708
CURRENT APPLICATION UNMBER: PCT/BP01/03971
PRIOR APPLICATION UNMBER: DE 10019058.8
PRIOR APPLICATION UNMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER: OF SEQ ID NOS: 98
SEQ ID NO 63
SEQ ID NOS: 98
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                                                     RESULT 8
US-10-995-561-13314/c
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US-10-240-708-63
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Best Local S
Matches 140
GENERAL
                   Sequence 13314, Application US/10995561 Publication No. US20050272054A1
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Publication No. US20050282157A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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les 140; Conserv
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                                                                                                                                                                                 TAGTTTATTTTCTCTTTATAAATAGA 879
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milarity 52.4%;
Conservative (
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Pred. No. 3.3;
0; Mismatches 126;
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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR APPLICATION NUMBER: US 60/243,096
FRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
FRIOR FILING DATE: 2000-11-20
FRIOR FILING DATE: 2000-11-20
FRIOR FILING DATE: 2000-11-30
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US-09-925-065A-803045
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CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13314

LENGTH: 119036
                                                                                                                                                                                                                                                                                                                        Sequence 803045, Application US/09925065A publication No. US20040181048A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
                PRIOR
PRIOR
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                FILING DATE: 2001-01-16
APPLICATION NUMBER: US 60/289,846
FILING DATE:
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Pred. No. 7.4;
0; Mismatches 188;
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                                                                                                                                                                      ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-240-708-11
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 803045
LENGTH: 488
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION UNMERS. DOCT/SP01/03971
                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-(NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: DE 10019173.8
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                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                               ENGTH: 6317
                                                                                                                                                                                                                                                                                    ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: DE 10032529.7
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: DE 10019173.8 FILING DATE: 2000-04-07
                    217
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                                               424 ACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACTCGA
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                                                                                              Conservative
                                                                                                           3.9%;
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                                                                                                           Score 51.6; DB 8;
Pred. No. 7.1;
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Best Local Simi
Matches 211;
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SEQ ID NO 242
LENGTH: 355211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(35521:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                    563 AATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAGCTATG
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683 TCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAGTCATTTTTAT 742
                                                                            623 ACGTTCAGATTTTCTTTTTCATTCTTGTTATTTTGTTATTTTTTTATATACATTTTCT
                                                                                                                                                                                                                                                                                                      443 ACAAGATTTAAAAAAAAATAACCAAAGTAACTAATCCACTCGAAAGCTATCATGTAATGTTT 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    660 TATTGTTTTATATACATTTTCTTCTTCTCACATAGAGTGATTTTCTTCCGATTTTATAA 719
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Similarity 46.1%;
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Pred. No. 18
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US-11-121-086-25
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APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC
FILE REFERENCE: 09138.6000-000000
FILE REFERENCE: 09138.6000-000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
SEQ ID NO 25
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.9%;
Best Local Similarity 45.5%;
Matches 219; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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                                                                             TGATTTTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAA 893
                                                                                                        ATATAATATGTTTATAATATATATATATATATTTTATATATATATGTTTATATATATATATATA 136897
                                                                                                                                 TTTTGTTATTGTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATT
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Best Local (
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TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (1)...(68741
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ilarity 46.2%;
Conservative
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RESULT 14
US-09-925-065A-667262
US-09-925-065A Application US/09925065A
; Sequence 667262, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nuclectide Polymorphisms in the Huma
; FILE REFERENCE: 108627.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-10-330-773-26
; Sequence 26, Application US/10330773
; Publication No. US20060040262A1
; GENERAL IMPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: NOVel Compositions and Methods in
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: US 60/243,096
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Pred. No. 25;
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RESULT 15
US-09-925-065A-667263
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PRIOR PRIOR DATE: 2000-11-30
PRIOR PRIOR DATE: 2000-11-30
PRIOR PRIOR DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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Best Local :
                                     APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
                                                                                                                                                                                                                                                                                             Sequence 667263, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens -09-925-065A-667262
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NG DATE: 2000-11-30
ICATION NUMBER: US 60/261,766
NG DATE: 2001-01-16
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Best Local Similarity 45.6
Matches 214; Conservative
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 667263
LENGTH: 677
TYPE: DNA
                                                                                                                                                   492 ATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAGCATATTT 551
909 TAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTAT 957
                                                                        849 АААТТАСТТТАТТТСТСТТТАТААААТАСААААСАСТТАСАААААТАСАСТТССССАСАС 908
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2 6/prodata/1/pubpna/US07 PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/US08 PUBCOMB.seq:*
3: /cgn2_6/prodata/1/pubpna/US09A PUBCOMB.seq:*
4: /cgn2_6/prodata/1/pubpna/US09B PUBCOMB.seq:*
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7: /cgn2_6/prodata/1/pubpna/US10E PUBCOMB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
WS-10-713-381-1
WS-10-713-381-2
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WS-10-425-113-4230
WS-10-425-114-23340
WS-10-425-114-123430
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Sequence 9, Appli
Sequence 3, Appli
Sequence 34230,
Sequence 134230,
Sequence 13464, A
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4.9	4.9	4.9	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.2	5.2	ა ა	5. 2
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GAC	ACC	CATE OF		6-6	h Similarity 11; Conser	GE 1, Applicatio ce 1, Applicatio ce 1, Applicatio ation No. US2004 L INFORMATION: CANT: ALBERTSEN CANT: HUFFWAN. CANT: GANKADAT, CANT: KENDALL, COF INVENTION: NO FINVENTION: NO FINUENTION NO REFERENCE: 578R NT APPLICATION NO FILING DATE: APPLICATION NO 1 3-381-1
GTA	GAGG	GIT	6 	IGIO	ity serv	Application U Application U Application U No. US2004022 ORMATION: ALBERTSEN, MA- FOX, TIMOTHY GARMANT, CAR HUPFWAN, GAR HUPFWAN, GAR KENDALL, TIMOTHY BAUCE: 578R ENCE: 578R BNCE: 578R BNCE: 578R BNCE: 1987- SNC DATE: 200 ICMION NUMBER NG DATE: 1997- SNC DI NOS: 1997- SNC DI NOS: 2878- SNC DI NOS: 2978- SNC DI NOS: 394 Patentin Ver. 394
9907	6—6 6—6				100 larity 100 Conservative	-391-1  te 1, Application US/10713381  tion No. US20040221331A1  INFORMATION  ANT: ALBERTSEN, MARC C.  ANT: GARMAT, CARL  ANT: GARMAT, CARL  ANT: KENDALT, TIMMY L.  OF INVENTION: MALE TISSUE-PH OF INVENTION: WSING SAME  EBERERUE: 578R  TR APPLICATION UNUMER: US/10/  TR PILING DATE: 1997-06-23  APPLICATION NUMBER: 08/880,4  RE: PATENTIN DATE: 2003-11-14  APPLICATION NUMBER: 08/880,4  RE: PILING DATE: 2003-11-14  APPLICATION NUMBER: 08/880,4  TRILING DATE: 2003-11-14  APPLICATION NUMBER: 08/880,4  TRILING DATE: 1997-06-23  ARE: PATENTIN Ver. 2.0  UNA  UNA  LISH: 280 ID NOS: 24  RE: DNA  AUSM: Zea mays  3-381-1
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CCAC	3-1	9 	CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAAC 	GAGT	Score 1311; Pred.~No. 6. Mismatches	A1 A1 SSUE-PREFERRED SAME 11-14 9/880, 499 23
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CGIC	CTGACCGAGGCCCATCAGACACCITTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 	CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCATC	CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAACTTCCACGGGTGCATGAT 	CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 	1394;	AND ?
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	GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT	مَ مَ
960	TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAAATTA 	9 9
900	TTCAAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT 	ón ón
840 840	TITCTGATTTTITAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTGATTTT	71
780 780	ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC	7 7
720 720	ATTGTTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCGATTT	6 G
660	TRATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT	6 6
600	CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAA 	<b>ດັ່ດ</b> ັ
540 540	CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA	4 4
89 89	TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACT	421 421
420 420	GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG	3 36
360 360	TTATTATTCTTTAGATATTATTTAATTTTTGGAAAAATAACAAACTTATACTTTTGTGTA 	3(
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Sequence 2, Application US/10713381

Sequence 2, Application Wo. US20040221331A1

GENERAL INFORMATION:
APPLICANT: ALBERTSER, MARC C.:
APPLICANT: FOX, TIMOTHY W.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHER TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381

CURRENT APPLICATION NUMBER: US/10/713,381

CURRENT APPLICATION NUMBER: 08/880,499

PRIOR APPLICATION NUMBER: 08/880,499

PRIOR FILING DATE: 1997-06-23

NUMBER OF SEQ ID NOS: 24

SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LEEGTH: 1394
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; ORGANISM: Zea mayв
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Best Local Similarity 100.0%;
Matches 1311; Conservative 0
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                                                                                         CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAA
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ATTGTTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA 720
                                 TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT
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Pred. No. 6.2e-275;
Mismatches 0;
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US-10-713-381-9
US-10-713-381-9
; Sequence 9, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
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                                                                                        ; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-9
               Query Match
Best Local Similarity
Matches 163; Conserv
                                                                                                                                                                    SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ALBERTSEN, MARC C. APPLICANT: FOX, TIMOTHY W. APPLICANT: GARNAAT, CARL W.
                                                                                                                                                                                                                         FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                             APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, CARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                        SOFTWARE: PatentIn Ver.
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                               12.3%;
               Score 160.6; DB 8;
Pred. No. 7.6e-25;
0; Mismatches 4;
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TYPE: DNA
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PRIOR APPLICATION NUMBER: 003-11-14

PRIOR APPLICATION NUMBER: 08/880,499

PRIOR FILING DATE: 1997-06-23

NUMBER OF EQ. ID NOS: 24

SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 158

TYPE: DNA
ORGANISM: Zea mays

US-10-713-381-3
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US-10-425-115-134230
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APPLICANT: ALBERTSEN, MARC C.

APPLICANT: FOX, TIMOTHY W.

APPLICANT: GARWAAT, CARL W.

APPLICANT: HUFFMAN, GARY

APPLICANT: KENDALL, TIMOTY L.

TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD TITLE OF INVENTION: USING SAME

FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 1134230
LENGTH: 1261
                                                                                                                                                                                                                                                   Sequence 134230, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La ROSa, Thomas J.
APPLICANT: Kovalic, David K.
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Best Local Similarity
Matches 157; Conserv
                                                                                                                         APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2003-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1274 GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1214 CAAGCCTTGCCTATTCTGAACCAAGAGGGATACCTACTCCCAAACCAATCCATCTTACTCAT 1273
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No. US200402217777
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cap invention: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
INVMBER OF SEQ ID NOS: 73128
SEQ ID NO 2334 0
LENGTH: 320
TYPE: DNA
ORGANISM: Zea mays
US-10-425-114-16264, Application US/10425114; Sequence 16264, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION: APPLICANT: Liu, Jingdong; APPLICANT: Zhou, Yihua; APPLICANT: Kovalic, David K.; APPLICANT: Screen, Steven E
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US-10-425-114-23340
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Publication No. US20040034888A1
GENERAL INFORMATION:
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Local Similarity 78.2%;
nes 97; Conservative
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Similarity 73.1%;
95; Conservative
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; Pred. No. 6e-0:
0; Mismatches
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APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

ITITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

ITITLE OF INVENTION: Plants

FILE REFERENCE: 38-21 (5322) B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 141826

LENGTH: 1326

TYPE: nv.
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; OTHER INFORMATION: Clone ID: LIB3062-023-G10_FLI
US-10-425-114-16264
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LENGTH: 624
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Best Local
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: MRT4577_60829C.1
                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
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nes 95; Conserv
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                                                                        816 GTTTCTTTCAAAGAATTTTGATTTTTCAAAAAAAATTAGTTTATTTTCTCTTTATAAAA 875
                                                                                                                                         756 TGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTTAAGAGCTAGTTTGGCAACCCT 815
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     TAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCTAGAAT 920
                                                                                                         TGAAGTTGGTGGTGTGCTGGTATTTCACCTTTAACTGTAAGGACTAATTTGGGAACCCA
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                                                                                                                                                                          Conservative
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Pred. No. 8.3e-06;
0; Mismatches 35;
                                                                                                                                                                                            Score 73; DB 8; Length 1326; Pred. No. 2e-05;
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RESULT 9
US-10-425-114-32493
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US-10-425-114-32493
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                                                                               US-10-425-115-83293
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Publication No. US20040034888A1
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Best Local Similarity 73.6
Matches 106; Conservative
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SEQ ID NO 83293
LENGTH: 2729
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CURRENT FILING DATE: 2003-04-28
                                       Query Match
Best Local Similarity 60. Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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:ENGTH: 2445
                                                                                                                                     PEATURE:
NAME/KEY: unsure
LOCATION: (1)..(2729)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                    ORGANISM: Zea mays
                                                                                               OTHER INFORMATION: Clone ID: MRT4577_175978C.1
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THE REFERENCE: 38-21 (52222)18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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Screen, Steven E
Tabaska, Jack E
Cao, Yongwei
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73.6%;
                     5.6%;
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Pred. No. 2.9e-05;
0; Mismatches 37;
; Score 72.8; D:
; Pred. No. 3.1e
0; Mismatches
                       DB 8;
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                                          Length 2729;
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US-10-425-115-51470/c
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US-10-425-114-17816/c
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                                                                                                                                  Sequence 17816, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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LENGTH: 1203
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Best Local
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/425,115
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: MRT4577_146936C.1
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LOCATION: (1)..(1203)
OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1189 ACTTTATTAAGGGCTAGTGGGGGAA-CATATTTTTCCAAAAAGATTTCTATTTTCTTAAA 1131
                                                                                                                                                                                                                                                                                                                                                                            1130 GAAAATTAGTTTATTTTCTCTTGGAAAAATAAAATCCCCGTAGAAAAATAGAGTTTCCAA 1071
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                                  Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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: Nucleic Acid Molecules and Other Molecules Associated With
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76.1%;
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Pred. No. 2.5e-05;
0; Mismatches 31; Indels 1
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TITLE OF INVENTION: Nucleic Acid Molecules and Oth TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 142853
LENGTH: 1123
TYPE: DNA ORGANISM: Zea mays
FEATURE:
RESULT 14
US-10-425-114-31957
; Sequence 31957, Application US/10425114
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US-10-425-115-142853/c
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 17816
LENGTH: 928
TYPE: DNA
ORGANISM: Zea mays
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Publication No. US20040214272A1
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Best Local Similarity
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihus
APPLICANT: Cao, Yongwei
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Similarity 78.0%;
99; Conservative
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                                                                                                                                                               AATTAGTTAATTTTCT
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                                                                                           ACCCCTA 696
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78.0%;
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Pred. No. 3e-05;
0; Mismatches 27; Indels
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Pred. No. 3.3e-05;
0; Mismatches 27;
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B.
APPLICANT: Screen, Steven B.
APPLICANT: Tabaska, Jack E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Otleitle Of Invention Number: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 31957
LENGTH: 2537
                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 52216
SEQ ID NO 52216
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; OTHER INFORMATION: Clone ID: MRT4577_147620C.1
US-10-425-115-52216
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US-10-425-115-52216
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Best Local Similarity
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                       TTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAG 911
                                                                                                          TTTAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTGATTTTTTCAAAAAAA
TTAGTTCATTTTTCCTTGAGAAAATAGGAATCCCTTAAAAAAATAGTGTTTTCAAACTAG
                                                                                                                                                                Conservative
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                                                                                                                                                                                   Score 71.8; DB 8;
Pred. No. 4.9e-05;
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Pred. No. 4.9e-05;
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                                                                                                                                                                                                        DB 8;
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## ALIGNMENTS

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121 CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157 	61 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG 120 	1 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC 60	Match 100.0%; Score 157; DB 6; Length 255; Local Similarity 100.0%; Pred. No. 5.6e-40; es 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="Zea mays" /organism="Zea mays" /mol_type="unassigned DNA" /db_xref="taxon:4577"	PIONEER HOUSENATIONAL, INC. (US) Location/Qualifiers	Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L. Male tissue-preferred regulatory region and method of using same parent. WO 0160097-A 9 23-ANG-2001;	Zea mays Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	AX224402 255 bp DNA linear PAT 10-SEP-2001 Sequence 9 from Patent WO0160997. AX224402 AX224402.1 GI:15554644

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PD 30-OCT-2001

PP 19-JUN-1998 JP 1999504910

PR 23-JUN-1997 US 08/880499

PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W PI TIMMY L KENDALL

PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C07K14/34, C12Q1/68, PC A01H5/00

CC Strandedness: Single; CC Topology: Linear; FH Key Total Profession Political Politics Profession Profession Politics Profession Politics Profession P
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Homo sapiens
Male tissue-preferred regulatory region and Patent: JP 2001520523-A 2 30-OCT-2001; PIONBER HI BRED INTERNATIONAL INC PN JP 2001520523-A/2
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1 (bases 1 to 1394)

Albertsen, M.C., Fox, T.W.,

Kendall, T.L.
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Mammalia; Eutheria;
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1 (bases 1 to 1394)

Albertsen, M.C., Fox, T.W.,

Kendall, T.L.
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BD062177.1 GI:22607782
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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23-JUN-1997 US 08/880499
MARC C ALBERGYSEN,TIMOTHY W FOX,CARL W GARNAAT,GARY A HUF
TIMMY L KENDALL
C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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PI MARC C ALBERTSEN
PI TIMMY L KENDALL
PC C12N15/82,C12N15
CC07K14/33,C12Q1/68,
PC A01H5/00
CC Strandedness: Si
CC Topology: Linear
FH Key
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Spermatophyta; Magnoliophyta; Liliopsida;
Clade; Panicoideae; Andropogoneae; Zea.
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CAACTTCCATGCAAACACGCACATATGTTTTCCTGAAC
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19-JUN-1998 JP 1999504910
23-JUN-1997 US 08/880499
MARC C ALBERTSEN, TIMOTHY W I
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AX224395 Sequence 2: AX224395 AX224395.1

REFERENCE AUTHORS TITLE

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Query Match Best Local S Matches 157

Similarity

100.0%; ilarity 100.0%; Conservative 0

157;

SOURCE

Zea mays Zea mays

KEYWORDS VERSION

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1215 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
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Zea mays male fertility protein
AF360356 GI:14028756
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Fox, T.W., Trimnell, M.R. and Albertsen, M.C.
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Pred. No. 5.6e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; hiliopsida; Poales; Poaceae; PACCAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX224396.1 GI:15554638
                                                                                                                                                                      Similarity
            CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT 120
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TGELYVADAYYGLMVVGQSGGVASSVAREADOEDFIRFAUDLDVHRNGSVFFTDTSMRY
SRKOHLMILLEGEGTGRLLRYDETSGVHVVLKGUFFENGVOLSEDHGFLLFSETTNG
RIMKYMLEGFRAAGEVEVFAALLGGFBUVRSNGRGQFWVALDCCRTPAQEVFAKRPWLR
TLYKFEDLSLKVLTWKAARRMHTVLALLDGBGRVVEVLEDRGHEVMKLVSEVREVGRK
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dyrpvkhelapygevmgswprdnasrlrrgrlefvgevegpesiefdlogrgpyagla
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gene="Ms45"
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Pred. No. 5.5e-40;
Mismatches 0;
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Pred. No. 2.1e-36;
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DESCRIPTION DESCRI	_type="genomic DNA" xref="taxon:39947" omosome="3" ne="0.71041F02"	,	Gaps	core 54; DB 15; ced. No. 1.8e-06; Mismatches 10;	34.4%; 85.7%; vative	h Simi 60;
DB 1520001 1510000  AC152566  AC152567  AC152566  AC15266  AC152666  AC15266  AC152	Location/Q 1137327 /organism=	FEATURES Source		010000 0710000		.P008209_195 .P008209_196
Discount 1310000  13100000  1310000  13100000  131	nucleotide sequence of this BAC clone was generated by combining Syngenta, Monsanto and Arizona Genomics Institute sequencing data.			510000	-,-,	P008209_193 P008209_194
1500001   1510000   1510	by a single subclone. Region 18678-18873 is a double stranded single subclone. Areas 6957-70761, 8936-90416, 98951-99009, 191316-196607 and 113165-113162 are covered by Monsanto colv. The			310000 ·		P008209_190 P008209_191
December   19500001   19500000   19500000   195000000   1950000000   195000000   195000000   195000000   195000000   195000000   195000000   195000000   195000000   195000000   195000000   1950000	restriction digest. There are transposons located at area 29427-32874 and at area 19945-33212. Region 70511-70536 is covered	·	•	010000		P008209 188
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B 350001 3510000  13510001 3110000  13710001 311	Jan 11, 2003 thi s sequence was f	COMMENT	:	1210000 1310000		P008209_181 P008209_182
135   13500001   13510000   135	Submission ted (16-APR-2	TITLE JOURNAL		910000		P008209_178 P008209_179
135   1350001   1351000	Yu.Y., Soderlund,C., Chen,M., Kim,H., Rambo,T., Henry,D., Thompson,S., Simmons,J., Thurmond,S.K.	AUTHORS		710000 710000		1 1
135   1350001   1310000	03 Forbes, Tucson, AZ 85721, USA 1 to 137327)	REFERENCE		410000		
135   1500001   13510000   1351	bmlssion (11-JAN-2003) Arizona Genomics Institute, University	TITLE /		7210000 7310000		
135   1350001   1310000   1310000   1310000   1310000   13100000   13100000   13100000   13100000   13100000   13100000   13100000   13100000   13100000   13100000   14100000	; 1 to 137327) 1 to 137327) 2 and Thomsen c	REFERENCE AUTHORS	-	7110000 910000		
135   13500001   1310000	-2002) Arizona Genomics Institute, University es, Tucson, AZ 85721, USA	JOURNAL		710000 810000		
135   13500001   13510000   135	Soderlund, C., Kim, HR., Rambo, T., a, K. and Thompson, S.	AUTHORS		510000 510000	,,, ,,,	
135   13500001   13610000   137	(v9-0c1-2002) AIIZONA SENOMICE INSCILUCE, UNIVERSILY 33 Forbes, Tucson, AZ 85721, USA 1 to 137327)	REFERENCE		\$210000 \$310000		
135   13500001   13610000   13710000   13710000   13710000   13710000   13810000   13910000   13910000   13910000   13910000   13910000   13910000   13910000   13910000   13910000   13910000   140	a, K. and Thompson, S.	TITLE				
135   13500001   13610000   13710000   13810000   13810000   13810000   13810000   13810000   13810000   13910000   13910000   13910000   140	d 1 to 137327) Yu.Y. Soderlund.C. Kim.HR. Rambo.T.	JOURNAL REFERENCE AUTHORS		610000 710000 810000		
135   13500001   13610000   13710000   13710000   13810000   13810000   13810000   13810000   13810000   13910000   13910000   13910000   13910000   13910000   140	Yu,Y., Soderlund,C., Kim,HR., Rambo,T., Currie,J. mic Sequence	AUTHORS		310000 410000 510000		
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135 13500001 13610000 137100000 13710000 137 13700000 13810000 138 13800001 13910000 139 13900001 13910000 139 13900001 14100000 140 14000001 14210000 141 14100001 14210000 142 14200001 14310000 144 14400001 14410000 145 14600001 14510000 145 14600001 14510000 146 14600001 14510000 147 14600001 14510000 148 14500001 14510000 149 14500001 14510000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14500001 14500000 140 14000001 14500000 140 14000001 14500000 140 14000001 14500000 140 14000001 14500000 140 14000001 14000000 140 14000001 14000000 140 14000001 14000000 140 14000001 14000000 140 14000001 14000000 140 14000001 14000000 140 14000001 14000000 140 140000000000	<pre>(Japonica cultivar-group) (Japonica cultivar-group) ridiplantae; Streptophyta; Embryophyta;</pre>	ORGANISM		1910000 1910000 1810000		P008209_147 P008209_148
135 13500001 13610000 137100000 137100000 137 13700000 13810000 138 13800001 13910000 139 13900001 13910000 139 13900001 14100000 140 14000001 14100000 141 14100001 14210000 142 14200001 14210000 143 14300001 14310000 144 14100001 14410000 145 DEFINITION OTYZA Sativa (japonica cultivar-group) chromosome 3 142 14300001 14410000 143 14310000 14410000 144 1410000 14410000 000 0000 0	5206.3 GI:2759697	VERSION KEYWORDS		510000 610000		P008209_144 P008209_145
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135 13500001 13610000 Db 136 13600001 13710000			The state of the s	1010000 1910000 1910000		P008209 137 P008209 138 P008209 139
	302 CCTCCATGCA 36293			0610000 0710000		P008209_135 P008209_136

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Query Match 34.4%; Best Local Similarity 85.7%; Matches 60; Conservative

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SAPDIDKKIRALKKKIRLAEAQVQGDPENLKPEQLEKMKKIEGMKEELKLLENKSSPA
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                                                                                                                                                                     SGKKMIP FASKITIKOAGODI INVEDEDMDSLÜAFERDPPLÖPVHVLYELEVTMPIH
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ASSCFHASLFESKOHERVOHELPEVTEKGOGTANLMTDKYRPETAAQVCGNSKHVKF
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                                                                                              39012.
                                                                                                                                    YLSSGALSLSAEDIGLLAQCSTFSDRRESETIIEQAIS"
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119439 CCTCCATGCA 119430
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                                                                       CCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 123
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Pred. No. 1.8e-06;
0; Mismatches 10;
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Castaway-like"

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REFERENCE
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Zea mays
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BX950854
                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                       Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. Male tissue-preferred regulatory region and method Patent: WO 0160997-A 6 23-AUG-2001, PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Sequence 6 from Patent WO0160997
AX224399
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AX224398
 BX950854.12 GI:58190604
                                          BX950854
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AX224399.1 GI:15554641
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5 from Patent WO0160997.
                                                                                                                                                                                                                          /mol_type="unassigned
/db_xref="taxon:4577"
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the this is found the longest good quality representation will be submitted.
                                                                                                                                                                                                                                                                                                                                                                                                            75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discovery system (Zhirong Bao and Sean Eddy, submitted), a beginning 'dar' were identified by Rick Waterman (Stephen lab, WashU). For further information see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
CH211-125M22 is from a CHORI-211 BAC library
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fish-help@sanger.ac.uk Clone requests:
On Jan 25, 2005 this sequence version r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat names beginning 'Dr' were identified by the Recon repeat
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-fish-help@sanger.ac.uk Clone requestes: clonerrequest@sanger.ac.uk
On Jan 25, 2005 this sequence version replaced gi:56368832.
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Actinopterygii; Neopterygii; Tele
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 171896)
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Contact: zfish-help@sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-125M22"
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AC104134
AC104134.4 GI:19551199
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Submitted (04-DEC-2001) Genome
University School of Medicine,
                 The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from
                                                                                                                                                           Mapping information for this clone was provided by Dr. Wes Warre Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                            all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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Submitted (30-APR-2005) Genome
University School of Medicine,
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Submitted (20-MAR-2002)
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Submitted (15-FEB-2002) Genome
University School of Medicine,
MO 63108, USA
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Waterston, R.H.
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Doebber, A., Haakenson, W. and Tomlinson, C.
The sequence of Homo sapiens BAC clone RP11-525L16
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                                                                                                                           SOURCE INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: H_NH0525L16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://genome.wustl.edu
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(http://www.resgen.com)
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                                                                               Frengen, E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA.; H_NH0525L16.2 This gene was based on gi(21361154) Continued from H_NH0450E09.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (join (67723.
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(FLJ25369), mRNA.; H_NH0525L16.1
This gene was based on gi(22749356)"
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/clone_lib="RPCI-11"
4046. _4309
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/chromosome="2"
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Boguslavkly, ..., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, J., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kartatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Menduim, J., Meneus, L., Mihova, T., Menga, V., Mirphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Neman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Vela, R., Simb, T., Simber, A. and Zody, M., Submitted, 101. Mbs. 101. Submitted (21-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 214946).

Birren, B., Nusbaum, C., Lander, B., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T. Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cho Collymore, A., Cook, A., Cooke, P., Corum, B., Dakrellano, K., Cooke, A., Cooke, A Nguyen, C., Nicol, K., Nolden, C., Pierre, N., Pierre, N., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., O'Neil, D., Oliver, J., Peterson, K., Fhunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C. Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. http://ftp.genome.washington.edu/RM/RepeatMasker.html Submitted (23-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Macdonald, P., Meldrim,J., Lindblad-Toh, K. repeats were identified using RepeatMasker: t, A.F.A. & Green, P. (1996-1997) Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: /note="<30 qual SNGL region" complement(2941. .3295) /rpt\_family="MER31B" /clone="RP11-86001" /clone\_lib="RPCI-11 Human Male BAC" complement(1...362) /rpt\_family="HAL1" complement(823...1431) /rpt\_family="LIMC5" complement (3307 organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" /chromosome="15" Location/Qualifiers note="single clone coverage" 320 Charles Street, Cambridge, MA 02141, USA 2003 this sequence version replaced gi:27877278 Karatas, A., Kells, C. Meneus, L., Mihova, T., Mienga Micol, R., Norbu, C., O'Connor, e="<30 qual SNGL region" http://www-seq.wi.mit.edu Genome Center Manning, J., Mac. Manning, J., Mac. Minga, V., Mac. Minga, V., Mac. Minga, V., Mac. Minga, V., Minga, Minga .3311) , Landers, T., Levine McCarthy, M., Naylor, J.,

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3601. .4006
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/rpt_family="MIR"
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                                                                                                                                                                               Assembly program: XGRP4; version 4.5
Assembly program: XGRP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 141058 bases at least Q40
Consensus quality: 141224 bases at least Q30
Consensus quality: 141289 bases at least Q20
Insert size: 141354; sum-of-contigs
Insert size: 151354; sum-of-contigs
Insert size: 15219; 10.9% error; agarose-fp
Quality coverage: 8.68x in Q20 bases; sum-of-contigs
Quality coverage: 8.12x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-JAN-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiriles: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 15, 2005 this sequence version replaced gi:56309949.
               * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
------ Project Information
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HTG; HTGS PHASE1; HTGS ACTIVEFIN; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio
Danio rerio
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/mol_type="genonic DNA"
/db_xref="taxon:7955"
/clone="DKEYP-86C9"
/clone_lib="DanioKeypilot"
1. 10378
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42428. .141554
/note="assembly_fragment:00621.0"
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10479 . .42327
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 The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH76340 standard; DNA; 255 BP.
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	ALIGNMENTS				
Aaf15843 Human pro	3 AAF15843	1478	18.1	28.4	. 45
		164702	18.2	28.6	44
Human	•	164702	18.2	•	43
Human	10 ADB87934	164702	18.2	28.6	42
3	8 ADB20845	164702	18.2	28.6	41
-	8 ACF62730	164702	18.2	28.6	40
	13 ABD32806_5	110000	18.2	28.6	39
	11 ACN45162	51615	18.2	28.6	38
Adx13304 Plant ful	13 ADX13304	3231	18.2	28.6	37
Plant	13 ADX11599	2160	18.2	28.6	36
Strepto	6 ABN67847	1860	18.2	28.6	35
σ	13 ADW26566	1522	18.2	28.6	34
Huma	10 ADD71973	1043	18.2	28.6	ω ω
x	4 AAS32893	778	18.2	28.6	32
Human	4 AAS32892	778	18.2	28.6	3
9 Bact	13 ADS57339	756	18.2	28.6	30
Ada68284 Arabidops	8 ADA68284	1500	18.3	28.8	29
	2 AAT42063_06	110000	18.6	29.2	28
ä	9 AAL62902	1475	18.6	29.2	27
Continuation (3 of	AAF22303		18.7	9	26
Adf00796 Bacterial	10 ADF00796	1185	18.9	9	25
	4 AAH13328		19.0	29.8	24
	10 ADD33404		19.1	30	23
	10 ADD33403	378	19.1	30	22
	5 AAH76335	30	19.1	30	21
tion (8 c	9 ADB12064_07	110000	19.2	30.2	20
					1.

mediating fertility in a male plant.	2 13
A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for	3 3 3
WPI; 2001-514772/56.	3 %
Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;	3 14 5
(PION-) PIONEER HI-BRED INT INC.	₹ ½ Ş
15-FEB-2000; 2000US-00504487.	3 % 5
13-FEB-2001; 2001WO-US004527.	3 4 5
23-AUG-2001.	9 9 5
WO200160997-A2.	3 2 5
Zea mays.	₹ ∞ 5
Ms45; male tissue; regulatory region; transcription; male fertility; hybrid seed; promoter; ds.	555
Z. mays Ms45 promoter fragment.	2 H :
29-0CT-2001 (first entry)	₹ ≒ !
AAH76340;	85

Example 5; Fig 8; 50pp; English.

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1 8
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ARX
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                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX07408
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                                                                                                                                                                                            Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2;
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157; Conserv
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               CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCCTTGTTCCATCGTCC
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                                                                                     Score 157; DB 4; -
Pred. No. 2.4e-42;
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Pred. No. 1.4e-42;
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maize; hybrid seed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
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                                                                                                                                                                                                                   CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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  CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
                                                                                                  AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG 120
                                                                                                                                                                            CGTGTCATCTCACATGCATACTACATGCTTCTTCAACCGTTCGTCCTTGTTCCATCGTCC 1214
                                                                   AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
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                                                                                                                                                                                                                                                                                     100.0%; Score 157; DB 2; 100.0%; Pred. No. 2.4e-42; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                232 G; 442 T;
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RESULT 5
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Matches 157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                          Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
              29-OCT-2001
                                     AAH76333;
                                                             AAH76333 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 46; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-514772/56.
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                                                                                                                           1275
                                                                                                                                                                        1215 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG 1274
                                                                                                                                                                                                                          1155 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCCTTGTTCCATCGTCC 1214
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                                                                                                                                                                                                AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG 120
                                                                                                                       CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
                                                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative 0;
              (first entry)
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Pred. No. 2.4e-42;
Mismatches 0;
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Best Local :
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           WO200160997-A2
                                  Zea mays.
                                                                                                                       29-OCT-2001
                                                                                                                                                AAH76334;
                                                                                                                                                                       AAH76334 standard; DNA; 158 BP.
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Similarity 100.0%;
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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 matissue preferred regulatory region from Z. mays
Ms45; male tissue; regulatory region; transcription; male fertility; hybrid seed; ds.
                                                                                                 Z. mays Ms45 male tissue-preferred regulatory region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
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Pred. No. 2.4e-42;
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RESULT 7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                         Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 47; 50pp; English.
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22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-033277P.
21-NOV-2001; 2001US-0332132P.
                                                               21-JUN-2002;
                                                                                                                WO2003008540-A2
                                                                                                                                          Oryza sativa
                                                                                                                                                                  agriculture.
                                                                                                                                                                                 ss; abiotic stress
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                                                                                                                                                                                                       stress-regulated promoter SEQ ID NO:17293
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                                                                                                                                                                                                                                                                                    standard; cDNA;
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                                                               2002WO-US019668
                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                              tolerance; transgenic plant; plant; cereal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 146; DB
Pred. No. 6.1e-
0; Mismatches
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                                                                                                                                                                                                                                                                                    ВP
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1. No. 6.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huffman G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising nucleotide sequences the MS45 gene useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polymucleotides. Also disclosed are methods for using the polymucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polymucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polymucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New stress-responsive nucleic acid, us responsiveness of a plant, e.g. cereal stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         responsiveness of a plant to an abiotic stress, such as cold stress, stress, osmotic stress or any of their combinations. The present seq is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 48; SEQ ID NO 17293; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moughamer
                                                                                                                                                                                                                              Ms45; male tissue; regulatory region; transcription; male fertility; hybrid seed; ds.
                                                                                                                                                                                                                                                                    mays Ms45 male
                                                                                                                                                                                                                                                                                                29-OCT-2001
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                                       Albertsen MC,
                                                                                          15-FEB-2000; 2000US-00504487
                                                                                                                    13-FEB-2001; 2001WO-US004527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                PIONEER HI-BRED INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCCATGCA
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T, Provart
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les. Also disclosed are vectors, expression cassettes, host
                                       Fox TW,
                                                                                                                                                                                                                                                                     tissue-preferred regulatory region fragment.
                                                                                                                                                                                                                                                                                                                                                     DNA;
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                                        Garnaat
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g. cereal, to
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D, Zhu T;
                                        Huffman
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                                        Kendall
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WPI; 2001-514772/56

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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the M845 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment upstream of the TATA box of a c. mays M845 male-tissue preferred regulatory region nucleotide sequence
                                                                                                                                                                                                                                                                                                            A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
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                                                                                                                                                                                                                                                               Claim 14; Page 32; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Albertsen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mays Ms45 male tissue-preferred regulatory region fragment.
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                                                                                                                                                                                                                                                                                                                                       comprising nucleotide sequences the MS45 gene useful for
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TTCTTTTTCTCACCTCCCTCTGATTTCTTTGTACCTCACTTTCATTTTGGCCTTTAAGTT 2833 TGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAG 86 Similarity

20.6%;

Score 32.4; DB: Pred. No. 2.5; 0; Mismatches

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Best Local S
Matches 40
                                                                  The invention relates to detecting atopic dermatitis or psoriasis comprising assaying the levels of expression of an indicator gene at a rash site and non-rash site of a person with atopic dermatitis or psoriasis, comparing these levels with those of a healthy person, and determining that if the levels of indicators are higher or lower, then this indicates the disease. Also included are a reagent for detecting atopic dermatitis or psoriasis, a kit for screening for treatments, a transgenic non human vertebrate animal models for the diseases, an agent for inducing the diseases in mice and a DNA chip for assaying for the indicator genes. The method is used for treatment, detection and animal models for research of atopic dermatitis and psoriasis. The present sequence is a Mouse atopic-dermatitis/psoriasis-associated EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting atopic dermatitis or psoriasis comprises expression of an indicator gene at a rash site and person with atopic dermatitis or psoriasis.
      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-214514/20
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14-MAY-2003; 2003JP-00136544.
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                                                      (expressed sequence tag).
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ni K;
   3267 BP;
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ilarity 100.0%;
Conservative
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1029 A; 658 C; 590 G; 990 T; 0 U; 0 Other;
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                   the 6213 antisense sequences given in the specification where expression (C) of the nucleic acid inhibits proliferation of a cell. Also included are: (C) a vector comprising a promoter operably linked to the nucleic acid (C) a vector comprising a promoter operably linked to the nucleic acid (C) encoding a polypeptide whose expression is inhibited by the antisense (C) nucleic acid; (2) a host cell containing the vector; (3) an isolated (C) polypeptide or its fragment whose expression is inhibited by the compoundation of the activity of a gene expression is inhibited by the compoundation; (7) identifying a compound that influences the activity of a gene in an operor required for C) the gene product or that has an activity against a biological pathway (C) required for proliferation, or that inhibits cellular proliferation (8) (C) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway (C) required for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an (C) compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of constitution of an organism. The antisense nucleic acids are useful for identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus mutans
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Trawick JD,
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Xu HH;
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCNN, ADRN, or AFD1 and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with development genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                              Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a se of a segment of chemically pretreated DNA of genes associated with
                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-587529/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preuss D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAR-2000; 2000WO-US007392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAC containing repeats from centromeres 1-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACCTAACCCATCTTCCAAATAAACACCC 8714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTACTCATGCAACTTCCATGCAAACACGC 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATC
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99US-0127409P.
99US-0134770P.
99US-0153584P.
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Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by the European Patent Office
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111

The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors,

the

construction

Page 321-335; 1449pp; English

DNA construct comprising a plant centromere, ably inherited michrosomes which can serve a of transgenic plant and animal cells.

ag useful fo

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Sequence 64415 BP;

18698

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13554 C; 13083 G;

18980 T; 0 U; 100 Other;

Sequence

79467 BP; 18256 A; 19684 C; 20062

G;

20204

7 0 ď,

1261 Other;

antibodies,

growth

factors

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The invention relates to recombinant carcinoma associated (CA) nucleic CC acid sequences from mouse and human (ADAQ1482-ADAQ03094), and to CC arcombinant carcinoma associated proteins (CAP) encoded by them. The CC invention also encompasses expression vectors and host cells comprising a CC Anucleic acid, a polypeptide (especially an antibody) that specifically comprise to the protein, and a biochip comprising CA nucleic acid or CC fragments thereof. The sequences of the invention were identified using CC oncogenic retroviruses, which insert into the genome of the host organism CC arrandom. Many of these do not carry transduced host encogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a CC direct consequence of the effects of proviral integration into host consequence of the effects of proviral integration into host carcinoma by determination of the sequence CC direct consequence of the effects of proviral integration into host carcinoma by determination of the sequence CC direct consequence of the effects of proviral integration in particular CC discussed or propensity to carcinoma by determination of the sequence CC tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The CC present sequence of the invention. Note: The complete sequence data for this sequence of the invention. Note: The complete sequence data for this cancercan in electronic format directly from WIPO at the printed specification, but was obtained on the complete sequence at the complete sequence at the complete sequence of the complete se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse Nfatc1 carcinoma associated gene, SEQ ID NO:1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostate; lymphoma; leukaemia; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1235; 245pp; English.
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ilarity 58.1%;
Conservative
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Pred. No. 26;
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Query Match Best Local Similarity

19.5%; ilarity 56.4%; Conservative

Score 30.6; I Pred. No. 28; 0; Mismatches

DB 9;

Length 79467;

Indels

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0

Matches

57;

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RESULT 15
ADB72455
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2001; 2001US-00798586.
23-CCT-2001; 2001US-00094113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse Nfatcl gene
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                                                                                                                                                                                                                                                                                                                        Sequence 79467 BP; 18256 A; 19684 C; 20062 G; 20204 T; 0 U; 1261 Other;
                                                                                                                                                                                                                                                                                                                                                     carcinomas, e.g. lymphomas, cancers, heaptasm, have gene of the invention. sarcomas. The present sequence represents a mouse gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 283; 2304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-239337/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2001; 2001WO-US051291.
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57; Conserv
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; neoplasm; adenocarcinoma; sarcoma; gene.
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   CTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTC 151
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CACACACACACACACACACACACACACAGCTTGTGGCTC 53879

Search completed: March 5, 2006, 18:11:42 Job time: 105.48 secs

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## GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

Title: US-1 Perfect score: 157 Sequence: 1 cg	Run on:	OM nucleic - nuc	
US-10-713-381-2_COPY_1155_1311 157 1 cgtgtcatctcacatggcatcgcacatatgtttcctgaac 157	March 5, 2006, 18:11:59 ; Search time 741.207 Seconds (without alignments) 9910.279 Million cell updates/sec	OM nucleic - nucleic search, using sw model	ריף/יושאיר (ר/ בססט באטריפאפומרוטא שרתי

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

<b>Q</b> γ	Query Match Best Local Matches 15	ORIGIN		source	FEATURES				JOURNAL	TITLE	AUTHORS		NISM	ß	ACCESSION	LOCUS DEFINITION	RESULT 1 CC656939/c
1 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC 60	Query Match 100.0%; Score 157; DB 9; Length 687; Best Local Similarity 100.0%; Pred. No. 2.2e-39; Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	methylation filtered genomic DNA library"	/db_xref="taxon:4577" /clone="zmMBMa0554D15" /clone_1ib="ZM 0.7 1.5 KB" /note="Vector:_p8C5K-; Site_1: HincII; 0.7-1.5 kb	1b8/ /organism="Zea mays" /mol_type="genomic DNA" /strain="B73"	Class: methylation filtered. Location/Qualifiers	Email: whitelaw@tigr.org Seq primer: TF	9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208	aw	Unpublished (2002)	Lakey, N.	. (Dases I to 667) Whitelaw C.A., Quackenbush, J., Van Aken, S., Utterback, T., Deemick A. Frager C. M. Huddman M. A. Redell J. A. Rohlfing T.,	yta; Magnoliophyta; Liliopsid icoideae; Andropogoneae; Zea.	Zea mays Eukarvota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		CC656939 CC656939.1 GI:32060231	CG55639 687 bp DNA linear GSS 19-JUN-2003 CGMDQ20TV ZM 0.7_1.5_KB Zea may8 genomic clone ZMMBMa0554D15, GENOMIC SULTYEY BEQUENCE.	

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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2002)
Other_GSSs: OG1AG08TH
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methylation filtered genomic DNA library"
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/strain="B73"
/db_xref="taxon:4577"
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GSS.
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     Martienssen, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 301-838-0208
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 963)

1 (bases 1 to 963)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Whitelaw,C.A., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Numberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 702)

Bedell, J.A., Budiman, M.A., Nunberg, A., Cittek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., Korf, I.F., Mabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                         CW324514 702 bp DNA linear GSS 31-OCT-2004 104 819 11477203 148 35910 078 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11477203, genomic survey
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                                                                                                                                                                                                                                                 Sorghum bicolor (sorghum)
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Location/Qualifiers
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Other_GSSs: OGWDQ20TV
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/mol_type="genomic DNA
/strain="B73"
/db_xref="taxon:4577"
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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100.0%; Pred. No. 2.4
tive 0; Mismatches
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No. 2.4e-39;
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Plate: 819 row: c column: 19
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 702.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 615 6979
Fax: 314 615 5975
                                                                                                                                                                                                                                                                             Sorghum bicolor (sorghum)
Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Enbryophyta; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicooideae; Andropogoneae; Sorghum.

1 (bases 1 to 296)
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296 bp DNA linear GSS 02-NOV-2004 febb001f170m16k0 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone febb001f170m16, genomic survey
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4041 Forest Park Ave,
                                                                                                                                                                              Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., Korf, I.F. Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and Martienssen, R.A.
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@criongenomics.com
Plate: febb001f170 row: m column: 16
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                                                                                                                                            Sorghum genome sequencing by methylation filtration places mind: 3 (1), el3 (2005)
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                                                                                                              Contact: Bedell JA
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/mol_type="genomic DNA"
/cultivar="ATX623"
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'clone="11477203"
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Pred. No. 3.9e-09;
0; Mismatches 5
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Class: methylation fi
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genomic survey sequence
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Kirkness, B. F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canida
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Canis familiaris
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Contact, Kirkness EF
Che Institute for Genomic Research
The Institute for Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                    The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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cultivar="ATx623"
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/mol_type="genomic DNA"
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Location/Qualifiers
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clone="fsbb001f170m16"
                                                              /clone lib="Dog Library"
/note="Site 1: BstXI; Libraries
peripheral blood"
                                                                                                                      /organism="Canis familiaris"
/mol_type="genomic_DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
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               24.1%;
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Pred. No. 0.00042;
0; Mismatches 10
               Score 37.8;
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                 DB 10;
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               Length 636;
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GSS.
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Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
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G11-25n6 DG11-kidney Canis familiaris cDNA 3', mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                           Mus musculus molossinus (Japanese wild mouse)
Mus musculus molossinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Thomas Schlueter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dog arrayTAG cDNA clone collection 
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schlueter, T., Hermanns, J., Weindel, M., Henrich, J. and Loebbert, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thomas.Schlueter@lionbioscience.com Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="kidney"
/dev stage="adult"
/lab_host="DH10B"
/clone_11b="DG11-kidney"
/note="Organ: kidney; Vector: Dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="Beagle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Canis familiaris"
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                                                                        GI:47977978
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Pred. No. 0.49;
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Oryza coarctata (Porteresia coarctata)
Oryza coarctata
Oryza coarctata
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 24.1%;
l Similarity 51.9%;
69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, (E-mail:hattori@gc.riken.jp, URL:http://hpp.gsc.riken.go.jp/, Tel:81-45-503-911), Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
                                                                                                                                                                           CZ727957 874
OC_Ba0055L24.f OC_Ba Oryza
5', genomic survey sequence.
CZ727957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library availability, please contact Kuniya Abe Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contribution of Asian mouse subspecies Mus musculus molossinus genomic constitution of strain C57BL/6J, as defined by BAC-end
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Shiroishi, T.
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Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CATATGTTTCCTG 154
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                                                                                                                                                                                                                                                                                                                                                                                        CAAACTTTTTTTG 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
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/clone_lib="MSMg01 Mouse Male BAC Li
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Pred. No. 0.57;
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大小のない まんかい

**美国教育等展现** 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB505306 RIKEN full-length enriched, 10 days lactation, adult female mammary gland Mus musculus cDNA clone D730002G06, mRNA
                                                                              Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, Y., Komon, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura Ohmo, M., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shisaki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahisaki, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 874)
Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Rod A. Wing
                                           Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                  BB505306.2 GI:16442791
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BACKWARD: CAC TCA TTA GGC ACC CCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTCCATGTA 846
                                                                                                                                                                                                                                                                       (bases 1 to 700)
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                                                                                                                                                                                                                                                                                                                                                        musculus
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                                                                                                                                                                                                                                                                                     ryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ilia; Butheria; Buarchontoglires; Glires; Rodentia;
rognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rwing@genome.arizona.edu
ry for Genome Exploration Research Group, RIKEN Genomic Center(GSC), Yokohama Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="OC_Ba"
/note="Vector: pAGIBAC1;
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/db_xref="taxon:77588"
/clone="OC_Ba0055L24"
/tissue_type="leaves"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Oryza coarctata"
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78.6%;
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                                                         this sequence version replaced gi:9514268.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KONDO, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Kalizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit on 
further details
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Numan Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                      contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="mammary gland"
dev_stage="10 days lactation, adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="D730002G06"
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                                                                                                                                                                                                                                                                    our web site (http://genome.gsc.riken.go.jp/) for
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Matches Query Match **Госат** 195 27 TGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAG 86 67; Similarity TTCTTTTTCTCCCCTCCCTCTGATTTCTTTGTACCTCACTTTCATTTTGGCCTTTAAGTT 254 Conservative 21.7%; Score 34; DB 2 Pred. No. 8.3; 0; Mismatches 0, 2; Length 700; 55 \* Indels 0;

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87 GATACCTACTCCCAAACATCCATCTTACTCATGCAACCTTCCATGCAAACACGCACATAT 146

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KEYWORDS
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COMMENT
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AUTHORS
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Callorhinchus milli
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Holocephali; Chimaeriformes; Callorhinchidae; Callorhinchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CW871670 734 bp DNA linear GSS 12-FEB-2005 she2h63-44.g 013.abl Whole-genome shotgun library of the elephant shark (aka elephant fish) Callorhinchus milii genomic, genomic
                                                                              CL026582 1677 bp DNA CH216-23G24_Sp6.1 CH216 Xenopus tropicalis CH216-23G24, genomic survey sequence.
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Institute of Molecular and Cell Biology
El Biopolis Drive, Singapore 138673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 734)
Venkatesh,B., Tay,A., Dandona,N., Patil,J.G.
A compact cartilaginous fish model genome
Curr. Biol. 15 (3), R82-R83 (2005)
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   Xenopus tropicalis (western Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Venkatesh B
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65 6779 1117
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genome shotgun sequences (
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/clone lib="Whole-genome shotgun library
shark (aka elephant fish)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Callorhinchus milii"
/mol_type="genomic DNA"
/db_xref="taxon:7868"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="Male"
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54.4%;
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                     clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bource
Hominidae; Homo.

E 1 (bases 1 to 440)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)

Tumor Gene Index

Unpublished (1997)

L Contact: Robert Strausberg, Ph.D.

Email: cgapbs--email.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Cen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69;
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                                                                                                                                                                                                                                                                                                                                         tr16b06.x1 NCI_CGAP_Ov23
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                  AI744861.1
EST.
                                                                                                                                                                                                                                                                                                                mRNA sequence
AI744861
                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                               Homo sapiens (human)
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GI:5113149

Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;

Project (CGAP),

Michael

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Local Similarity
                                                                                                               889 TCTTCCAT 896
                                                                                                                                                   123 ACTTCCAT 130
                                                                                                                                                                                                                            63 GCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Submissions@watson.wustl.edu
Insert Length: 175000 Std Error:
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1677)

Kremitzki,C., Carter,J., McPherson,J., Warren,W., Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Sequencing Center
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2003)
                 AI744861
                                                                                                                                                                                         TCATCAACTATTCTTACAGTTCATGTCACCTCCTCTCACTTTCTATATATTATTCAGACA 888
                                                                                                                                                                                                                                                                                                        TGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAA 62
                                                                                                                                                                                                                                                                  TGTCGTCTCACATGCACTTACTCCTGATTCTTTTGCTCTTCTACATGTGTCCATCCGGTT 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence start: 125 quality sequence stop: 217.
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell line="Stock 248 F7A2,
/clone lib="CH216"
/note="Vector: pTARBAC2.1; (BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-23G24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Xenopus tropicalis"

/mol_type="genomic_DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1677
                                                                                                                                                                                                                                                                                                                                                                21.4%;
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Pred. No. 15
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440 l
Homo
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 sapiens
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mRNA
ens cDNA
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 linear
A clone I
                                                                                                                                                                                                                                                                                                                                                                                  Length 1677;
                                                                                                                                                                                                                                                                                                                                                Indels
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r EST 21-JUN-1999
IMAGE:2218451 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Graves, T.
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                Gaps
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FEATURES

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319 TCCATCTTAATTAAACAGCGTCGATGTCTGCCTAGATATCTGTTTCCT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 TCCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 CTTTGGCCAGCAAACTAGTATATCATATTCCTCCCCAAAGCAACACCTCCTACTTTATTT 318
                   Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert. Poly-A: Based upon the presence of a run of 14 or more T residues
                                                                                                                                                                                                                         Email: cdna@jgl.psf.org
Email: cdna@jgl.psf.org
Tissue Procurement: Richard M. Harland Laboratory, University of
California, Berkeley: http://tropicalis.berkeley.edu/home
CDNA Library Preparation: Richard M. Harland Laboratory, University
                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2004)
Other ESTS: JGI XZG22009.fwd
Contact: Lindquist, E.A., Rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 CTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAA 105
                                                                                                                                                  http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                  DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CX446438 648 bp mRNA linear E JGI XZG22009.rev NIH XGC_tropGas7 Xenopus tropicalis IMAGE:7537449 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CX446438.1 GI:57262270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C., Srokstein, P. and Lindquist, E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Richardson, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amphibia; Batrachia; Anura; Mesobatrachia;
Kenopodinae; Xenopus; Silurana.
| (bases 1 to 648)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/hage.html seq primer: -40UP from Gibco
                                                                                                                                                           [ California, Berkeley
NA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
lone_Distribution: I.M.A.G.E. Consortium/LLNL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1 sall;
Site_2: Not!; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All rare primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Institute Xenopus tropicalis EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="tumor, 5 pooled (see description)"
/lab host="DHIOB"
/lab host="NOI_CGAP_Ov23"
/clone lib="NOI_CGAP_Ov23"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site 1:
Site_2: NotI; Cloned unidirectionally. Primer: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="IMAGE:2218451"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence stop: 411.
ation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32.8; DI
Pred. No. 18;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Richardson, P.
this clone was polyadenylated.
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ORGANISM
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VERSION
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CW558661/c
                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50;
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SOURCE ORGANISM

VERSION KEYWORDS ACCESSION

CX446438/c DEFINITION

밁

Matches Query Match

61;

REFERENCE

TITLE AUTHORS

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586 TTTGAATTÁTGAAAAGGCCATCTCCCATAGACTCCATTTTAGGCAAGTAATTTCCATTTT 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          526 AAAAAGTATTTTTTTCC 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 AACACGCACATATGTTTCC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 ГСТБААССАВБАБАТАССТАСТСССАВАСЬАТССАТСТТАСТСАТБСАВСТТССАТБСА 133
                                                                                                                                                                                                                                                 Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036,
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza australiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CW558661 740 bp DNA linear GSS; OA_ABBA0080B07.f OA_ABBA OFFIca a ustraliensis genomic clone OA_ABBA0080B07.5', genomic survey sequence.
                                                                                                                                                           FORWARD: TAA TAC GAC TCA CTA TAG
BACKWARD: CAC TCA TTA GGC ACC CC
                                                                                                                                                                                                                                                                                                                                                                       Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ebkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza australiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CW558661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CW558661.1 GI:54424196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                   te: 0080 row: B column: 07
primer: TAA TAC GAC TCA CTA TAG GG
ss: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 740)
                                                                                                                                                                                                              PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                 rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yu, Y.
organism="Oryza australiensis"
| mol_type="genomic DNA"
                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_XGC_tropGas7"
/note="Vector: pCS108; Site 1: Sall; Site 2: NotI;
Gastrula library constructed by Russell B. Fletcher in R.
Harland's lab using poly A RNA and oligo dT primers
(Invitrogen SuperScript Plasmid System for cDNA Synthesis
and Cloning). Sall [5' end) -NotI (3' end) cDNA was
inserted into vector pCS108
(http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Xenopus tropicalis"
/mol_type="mRNA"
/db xref="raxon:8964"
/clone="IMAGE:7537449"
/tissue_type="whole embryo"
/tissue_type="whole embryo"
/dab_nost="E. coli XLI-Blue derivative, Stratagene
                                                                                                                                                                                                                                                                                                                                                                                                                                     Muller, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryzeae;
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Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  ., Yost,D., Rao,K., Luo,M., Jetty,R., Hatfield,J., Soderlund,C. and Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza.
                                                                                                                                                              CCA
                                                                                                                                                                                   ရှ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 8;
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                                                                                                                                                                                                                                                                                                 USA
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Run

on:

nucleic search, using sw model

GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration

March 5, 2006, 21:54:12;

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 8

summaries

Database

Issued\_Patents\_NA:\*

/cgn2\_6/ptodata/1/ina/1\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/5\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
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/cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
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/cgn2\_6/ptodata/1/ina/BCCTUS\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/BCCTUS\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/BCCMB.seq:\*

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Match Length DB

Description

US-08-880-499-1 US-08-880-499-2 US-09-949-016-16073 US-09-543-681A-1081

1830121 1830121 1830121 164190 64190 11022 11022 11025 11490 11495 12472 22472 22472 22472 22472 3014 3014 3588

3 US-09-557-8841
3 US-09-643-990A-1
3 US-10-158-865-1
3 US-10-158-865-1
3 US-09-949-016-14712
3 US-09-949-016-15502
3 US-09-949-016-15502
3 US-09-949-016-11407
3 US-09-949-016-11407
3 US-09-949-016-12610
3 US-09-949-016-12610
3 US-09-949-016-1279-1813
3 US-09-9170-279-1813
3 US-09-710-279-1813
5 US-09-710-279-3680

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

1303057 seqs, 888780828 residues

Scoring table:

IDENTITY NUC Gapop 10.0 ,

Title: Perfect score:

US-10-713-381-2\_COPY\_1155\_1311 157

cgtgtcatctcacatggcat.....cgcacatatgtttcctgaac 157

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                Sequence 1, Appli
Sequence 16073, Ap
Sequence 16073, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 17172, A
Sequence 1712, A
Sequence 17413, A
Sequence 17440, A
Sequence 17440, A
Sequence 37, Appl
Sequence 1813, Ap
Sequence 3747, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: 107...
COUNTEX: USA
ZIP: 50131
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,499
PTITING DATE: CONCURRENTLY HEREMITH
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US-08-880-499-3
                                                                         ; MOLECULE TYPE: DNA (genomic) US-08-880-499-1
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Query Match
                                                                                                                                                                                                                                                                                 TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADUAL STREET: DOX 1000 CITY: JOHNSTON TOWN THE IOWN USA
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Darwin Building, 7100 N.W. 62nd Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Albertson, Marc C. APPLICANT: Fox, Tim W.
                                                                                                                                                                           LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08880499
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            100.0%; Score 157;
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3 US-09-949-016-11979
3 US-09-949-016-11976
3 US-09-949-016-11989
3 US-09-949-016-11713
3 US-09-949-016-11713
3 US-09-949-016-12088
3 US-09-949-016-13037
3 US-09-949-016-13037
3 US-09-949-016-15039
3 US-09-949-016-12928
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949-016-17368
949-016-14091
949-016-13779
949-016-17576
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Sequence
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17378, A
14001, A
13776, A
17776, A
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US-08-880-499-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
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Patent No. 6037523
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                                                                                                                                                       Query Match
Best Local Similarity
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TOPOLOGY: line
MOLECULE TYPE:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                              NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/880,499 FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: 800
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TELEFAX: (515) 248-4844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O
1215
                                                                  1155
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                  AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                                      CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCCGTTCGTCTTGTTCCATCGTCC
AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                  CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC 1214
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Huffman, Gary A.
                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                          single
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) 248-4844
) NO: 2:
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                                                                                                                                                     Score 157; DB 3;
Pred. No. 9.4e-44;
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                                                                                                                                       Mismatches
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                                                                                                                                                                    Length 1394;
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; LOCATION: (1)...(385136)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-16073
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                                                                                                                    ; ORGANISM: Proteus mirabilis US-09-543-681A-1081
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                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: GARY BRETON
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT PLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16073, Appendix Patent No. 681233
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Best Local Similarity
                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                          Best Local
                                                                            Query Match
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 385136
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35 CAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTA 94
                                                                                                                                                                                  1185
                                       l Similarity
50; Conserv
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                                         Conservative
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                                                          18.9%;
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Pred. No. 14
                                                            Score 29.6;
Pred. No. 3.
                                       ed. No. 3.4;
Mismatches
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RESULT 6
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-557-884-1
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 67; Conserv
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Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischman
TITLE OF INVENTION: T
                                                                                                                                                                                                                                                                    677275 ACTTRAATTCAGCCTGCTTGCTTGCTATTGCATTTGCATTAAATGCAAGCATAGCCT 677216
                                                                                                                                                                                       677215
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMPUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                72 ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                       APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09557884
                                                                                                      CAACCAACCA 677146
                                                                                                                                               CAAACACGCA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell pentium
COPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WAME: Michelle S. Marks
                                                                                                                                                                                                                                                                                                                                                       18.6%; ilarity 51.5%; Conservative
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                                                                                        Patent No.
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Patent No. 6528289
GENERAL INFORMATION:
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Best Local Similarity
Matches 67; Conserv
Patent No. 6846651
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:

COMPUTER: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                   OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fragn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                             132 CAAACACGCA 141
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FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                   Application US/10158865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 301-610-57,90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/643,990A FILING DATE: 23-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1830121 base pairs
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REGISTRATION NUMBER: 40,302
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FILE REFERENCE: PB186P2C1D1
CURRENT APPLICATION NUMBER: US/10/158,865
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR APPLICATION NUMBER: US 08/476,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21 NUMBER OF SEQ ID NOS: 1 SOFTWARE: PatentIn vers SEQ ID NO 1 LENGTH: 1830121 NAME/KEY: misc\_feature LOCATION: (40808)..(40) OTHER INFORMATION: n e NAME/KEY: misc feature LOCATION: (10150)..(10150) OTHER INFORMATION: n equals FEATURE:
NAME/KEY: misc\_feature
LOCATION: (9921)..(9921)
OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (36636)..(36636) OTHER INFORMATION: n equals LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals ORGANISM: Haemophilus influenzae NAME/KEY: misc\_feature LOCATION: (45732)..(45732) OTHER\_INFORMATION: n equals NAME/KEY: misc feature LOCATION: (45593)...(45593) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (44975)...(44975) OTHER INFORMATION: n equals LOCATION: (44416)..(44416) OTHER INFORMATION: n equal NAME/KEY: misc\_feature LOCATION: (36551)..(36 NAME/KEY: misc\_feature LOCATION: (36543)..(36543) OTHER\_INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (29298)..(29298) OTHER\_INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (4747)..(474 FEATURE: NAME/KEY: misc\_feature NAME/KEY: misc\_feature OCATION: (47036)..(47036)
OTHER INFORMATION: n equals a,t,c, THER INFORMATION: n equals DAME/KEY: misc\_feature DOCATION: (44905)..(44905) PatentIn version 3.1 n equals n equals Thereof, and Uses Thereof (40810)a,t,c, a,t,c, a,t, a,t,c, a,t,c, a,t,c, a a,t,c, g) a,t,c, a,t,c, a,t,c, a,t,c, ŗ ŗ ò ò ò or ದ್ದ õ õ or 9 ç ç ö မ္ပ or or P မ္ပ 9 g Q ω ŧΩ ιο ω ω Q ω ω g ω ω

NAME/KEY: misc feature LOCATION: (80074)..(80024) OTHER INFORMATION: n equals FEATURE:
NAME/KEY: misc\_feature
LOCATION: (65309)...(65309)
OTHER INFORMATION: n equals FEATURE:
NAME/KEY: misc\_feature
LOCATION: (55369)...(55369)
OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (51805)...(51805) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (51602)..(51602) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (51334)..(51334) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (121344)..(121344) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (119750)..(119750) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (107248)..(107248) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (105121)..(105121) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (100091)..(100091) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (51786)..(51786) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (120038)...(120038) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (119924)..(119924) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (117136)..(117136) OTHER\_INFORMATION: n equals LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (122167)..(122167) OTHER\_INFORMATION: n equals OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (102696)..(102696) NAME/KEY: misc\_feature FEATURE: FEATURE: FEATURE: AME/KEY: misc\_feature 9,4 a,t, a,t,c, a,t,c, a,t,c, a,t, a,t,c, a,t,c, a,t,c, a,t,c, a,t,c, a,t,c, α a,t,c, g a,t,c, a,t,c, a,t,c, , t, c, 'n ò ò ò õ ę မ္ပ 9 ç or 얹 ဝူ õ õ 유 ဝူ 유 õ õ 유 8 ö Ø ιQ ω ø Q g ω g ω ω Q Q ω ω g ω ω

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RESULT 8
US-09-949-016-14712/c
; Sequence 14712, Application US/09949016
; Patent No. 6812339
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
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OTHER INFORMATION: n equals a,t,c,
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LOCATION: (140398)..(140398)
OTHER_INFORMATION: n equals
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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LOCATION: (131360) . (131360)
OTHER INFORMATION: n equals
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LOCATION: (131340)..(131340)
OTHER_INFORMATION: n equals a,t,c,
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OTHER INFORMATION: n equals a,t,c,
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LOCATION: (142750)...(142750)
OTHER INFORMATION: n equals
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LOCATION: (145171)...(145171)
DTHER INFORMATION: n equals a,t,c,
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JOCATION: (150841)...(150841)
THER INFORMATION: n equals a,t,c,
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OCATION: (147197)..(147197)
THER INFORMATION: n equals a,t,c,
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LOCATION: (145942)...(145942)
THER INFORMATION: n equals a,t,c,
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LOCATION: (145058)..(145058)
DTHER INFORMATION: n equals a,t,c,
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l Similarity 51.5%;
67; Conservative
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Pred. No. 63
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US-09-949-016-14712
                                   RESULT 10
US-09-949-016-15502
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; ORGANISM: Human
US-09-949-016-14713
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SEQ ID NO 14713
LENGTH: 64190
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SEQ ID NO 14712
Sequence 15502, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                 Query Match
Best Local (
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Best Local
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/241.755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 CTCATGTAACAT 284
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                                                                                                                                                115 CTCATGCAACTT 126
                                                                                                                                                                                        355 TCATCCAATAGTTTCCACTACTAATCCATGATGGAACTGAGTACTAATCAAGCCAATATT 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                           55 TCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTA 114
                                                                                                                                                                                                                                                                45;
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                                                                                                               CTCATGTAACAT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                 18.3%;
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                                                                                                                                                                                                                                                                                    Score 28.8;
Pred. No. 27;
                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                     Length 64190;
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GENERAL INFORMATION:

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LENGTH: 11022
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15502
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US-09-949-016-17447
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15592
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Best Local Similarity
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SECTION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SECTION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                             SEQ ID NO 17447
                                                                                                                                                               Matches
                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                       ENGTH: 41815
                                                                                                                                                                                Local Similarity
33118
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                                    122 AACTTCCATGCAAACACGCACATA 145
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                                                                                                                  AGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGC 121
ATGTCACATAGAGACATGCATGTA 33141
                                                                              AGACATGCAGATTCACACACATCCGCATAGCTGCTCCTACGGATCCCTGGTCACTCATTC
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63.2%;
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0; Mismatches
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                                                                                                                                                                                                     DB 3;
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                                                                                                                                                                                                     Length 41815;
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RESULT 12

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 191201
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Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 14149
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 601
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                     LENGTH: 11490
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                                                                                 5642 CAGGGCCTCTGCTTCCCTGCCCCTCCCCCTGCCCCCACCTCACCAGGAGGAAGCCCACGC 5583
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                                       98 CCANACANTCCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAA 156
                                                                                                                             8
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  CCTTGCACACCTGATGCCACATCCGCTTGAGTGGCAGGCGAGTGAAGATGTTGCCCCAAA
                                                                                                                             CCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTC 97
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58.0%;
                                                                                                                                                                                        17.7%;
52.1%;
                                                                                                                                                                    Score 27.8; DB Pred. No. 32; 0; Mismatches
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                                                                                                                                                                    0;
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                                                                                                                                                                                                              DB 3;
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US-099-949-016-16740, Application US/09949016
Sequence 16740, Application US/09949016
Frant No. 6812339
                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence; No. 6846621e; OTHER INFORMATION: synthetic construct
US-09-937-862B-37
                                      Query Match 17.6%; Score 27.6; I Best Local Similarity 55.1%; Pred. No. 15; Matches 54; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.7%;
Best Local Similarity 59.5%;
Matches 47; Conservative
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CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                               MALOR APPLICATION NUMBER: 60/127,464
RIOR FILING DATE: 1999-03-31
UMBER OF SEQ ID NOS: 89
OFWARE: FASTSEQ for Windows Version 4.0
ID NO 37
ID NO 37
                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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IE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

LE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

E REFERENCE: CLOO1307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 CCATGCAAACACGCACATA 145
53 CATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 TGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 TGTCAACCGTGATCCAACAGTATAATTAGTTCTTAGGAATTCCTCTCTCACAGGTAACTA 129
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G DATE: 2000-09-08
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Pred. No. 35;
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                                                                                  DB 3; Length 927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 14952;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                      Gaps
                                      0
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Db 551 CATCATCAAACCCCTCAATATTCTACACCTATGGAACAGGACCCACGAGAATTTCGATCC 610

Oy 113 TACTCATGCAACCTTCGATGGAACACGCACATATGTTT 150

Search completed: March 5, 2006, 22:36:28
Job time: 46.8947 secs

B

611 CTTTTGTGGGCATTACAAACGCGTACTCACATTTTTAT 648

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# OM nucleic - nucleic search, using sw model GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd. · 一大學 · 一大

Run on: March 5, 2006, 23:29:31; Search time 225.751 Seconds (without alignments) 5750.985 Million cell updates/sec.

Title: Perfect score: Sequence: US-10-713-381-2\_COPY\_1155\_1311 157

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0 1 cgtgtcatctcacatggcat.....cgcacatatgtttcctgaac 157

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

19587084

9793542 seqs, 4134689005 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
2: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
4: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
6: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
9: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
9: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
10: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Regult No.	Score	% Query Match	% Query Match Length	DB	ID	Description
ш	157	100.0	255	8	US-10-713-381-9	Sequence 9, Appli
N	157	100.0	1394	В	US-10-713-381-1	ب ب
ω	157	100.0	1394	8	US-10-713-381-2	Sequence 2, Appli
4	146	93.0	158	8	US-10-713-381-3	ω
5	50	31.8	50	œ	US-10-713-381-5	Sequence 5, Appli
σ	40	25.5	40	œ	US-10-713-381-6	6
c 7	32.2	20.5	399	œ	US-10-674-124A-9081	90
	31.6	20.1	2352	7	US-10-282-122A-36272	
9	31.4	20.0	565	4	US-09-925-065A-871704	
c 10	30.8	19.6	601	4.	US-09-925-065A-778732	
c 11	30.8	19.6	1122	7	US-10-437-963-1496	Sequence 1496, Ap
12	30.6	19.5	559	v	US-10-027-632-244811	244811
13	30.6	19.5	559	σ	US-10-027-632-244811	
14	30.6	19.5	79467	7	US-10-052-482-223	Sequence 223, App
15	30.4	19.4	52001	7	US-10-317-273-11	
16	30.2	19.2	436	4.	US-09-925-065A-153052	1530
17	30.2	19.2	1266	9	US-10-501-282-2923	Sequence 2923, Ap
18	30.2	19.2	1754382		US-10-501-282-6651	e 6651,
19	30	19.1	30	œ	US-10-713-381-4	
20	30	19.1	843	v	US-10-027-632-170626	Sequence 170626,
21	30	19.1	843	σ	US-10-027-632-170626	Sequence 170626,
22	29.8	19.0	236	w	US-09-783-590-10490	
23	29.8	19.0	617	4	US-09-925-065A-285326	Sequence 285326,

RESULT 2 US-10-713-381-1 ; Sequence 1, Application US/10713381 ; Publication No. US20040221331A1

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28.8 28.8 8	229 299 299	29.2 29.2 29	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	29.8
18.3	18.5 18.5 18.5			19.0
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44 D) D)	70000	۵ <sub>9</sub> ۵	07 65 65 4	441
US-09-925-065A-805392 US-10-027-632-21721 US-10-027-632-21722	US-10-027-632-222444 US-10-027-632-222445 US-10-027-632-222444 US-10-027-632-222445 US-10-027-632-222445	US-10-158-865-1 US-10-981-687-1 US-10-425-115-78606	US-09-925-065A-12385 US-10-027-632-254612 US-10-027-632-254612 US-10-027-632-254612 US-10-027-632-179264 US-10-027-632-179264 US-10-027-632-199264 US-10-321-802-11 US-10-321-802-11 US-10-329-670-1	US-09-925-065A-285327 US-09-925-065A-285328 US-10-424-598-57018
Sequence 805392, Sequence 21721, A Sequence 21722, A	Sequence 222444, Sequence 222444, Sequence 222444, Sequence 222445, Sequence 85365, A	Sequence 1, Appii Sequence 1, Appli Sequence 78606, A	17 117 17 17 17 17 17	285327, 285328,

# ALIGNMENTS

용 성	망양	유 왕	<b>3</b> w 0	US-
		•	Query Match Best Local Matches 15	US-10-713-381 US-10-713-381 Sequence 9, Publication GENERAL INF APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT APP
121 C	61 A 75 A	15 0	Match Local Similarity Es 157; Conser	
CAÁCTICCATGCAAACACGCACATATGTTTCCTGAAC 	AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG 	CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC	milari Cons	e to partentable
CATGO	GCCTA	TCTCA	vat	USING MANAGER TO SEE TO MANAGER TO SEE TO MANAGER TO SEE T
AAACAC        AAACAC	TTCTGA	CATGGC        CATGGC	100.0%; 100.0%; ive	lication US/107133 US20040221331A1 TION: BETSEN, MARC C. X, TIMOTHY W. RNAAT, CARL W. FEMAN, MALE TISSUE- TION: MALE TISSUE- TION: MALE TISSUE- STAR WHOBER: US/1 DATE: 2003-11-14 ION NUMBER: 08/880 ATE: 1997-06-23 ID NOS: 24 ntIn Ver. 2.0 mays
GCACAT	ACCAAC       ACCAAC	ATACT/	30 24 08	/10713381 331A1 331A1 W. C. W. W. S. SAME G. S
TTCCATGCAAACACGCACATATGTTTCCTGAAC 	BAGGAT	ACATGC	Score 157; Pred. No. 2. Mismatches	on US/10713381 40221331A1 40221331A1 40221331A1 40221331A1 40221331A1 40322 40321 40322 403211-14 40422 4042 4042 4042 4042 4042 4042 4
TCCTGA	ACCTAC        ACCTAC	TIGITO	7; DB . 2.1e ches	
AC 157 	TCCCA.	AACCG	8; -43; 0;	REGULATORY
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	TTACT	CCATC	0;	
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GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 157; Conservative 0
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                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1394
TYPE: DNA
ORGANISM: Zea mays
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ORGANISM: Zea mays
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61 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                                         1 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCCTTGTTCCATCGTCC 60
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Pred. No. 3.8e-43;
); Mismatches 0;
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; SOFTWARE: PatentIn Ver. ; SEQ ID NO 5; LENGTH: 50; TYPE: DNA; ORGANISM: Zea mays US-10-713-381-5
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US-10-713-381-5
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/10713381 Publication No. US20040221331A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 157; Conserv
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SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, App. Publication No.
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                                                                                                                                                                                                                                APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                            CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMOY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
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99.4%;
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Pred. No. 1e-39;
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CURRENT APPLICATION NUMBER: US/10/674,124A
CURRENT FILING DATE: 2003-09-26
CURRENT ADDITION OF THE CONTROL OF THE
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OTHER INFORMATION: chr5.fa.O7frz.139538206
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIOR APPLICATION NUMBER:
RIOR FILING DATE: 1997-0
                                                                                                 GANISM: Homo sapiens
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LE OF INVENTION: USIN
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP2002-383869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP2000-112699
FILING DATE: 2000-04-13
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No. US20040221331A1
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Sequence 36272, Application US/10282122A
Publication No. US:0040029129A1
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                                                                       Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
ORGANISM: Streptococcus mutans
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nes 52; Conserv
                                                                                                                                               APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                    CATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                            CATION NUMBER: 60/242,578
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DATE: 2000-0
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Yamamoto, Robert
Forsyth, R.
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IG DATE: 2003-02-20
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Pred. No. 1.6;
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; Sequence 778732, Application US/09925065A
; Publication No. US20050228172A9
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-36
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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US-09-925-065A-871704
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                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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ORGANISM: Homo sapiens
-09-925-065A-871704
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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             PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
                                                                                                CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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APPLICATION NUMBER: US 60/250,092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCTCTTGCTTGGAAGAGCCCATGCTTGGTTTAACGCCCTTCTGTCTCCGTCTTGAAAT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAG
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58.5%;
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; Pred. No. 3.4;
1; Mismatches
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Pred. No. 4.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.4:
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 30-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 1496
LENGTH: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-778732
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 778732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
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Publication No. US20040123343A1
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Best Local Similarity
                                                                                                                               Best Local Similarity Matches 56; Conserv
                                                                                                                                                            Query Match
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PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT4530_101357C.1
                                                                                                                                                                                                                             ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                            120 GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
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                                                                                               60 CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT 119
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TCAGATCCACAAATCGCACCCTCCCATATCTGCTGAAC 216
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nilarity 57.1%;
Conservative
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Pred. No. 5.
                                                                                                                                                Score 30.8;
Pred. No. 7
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RESULT 12 US-10-027-632-244811 ; Sequence 244811, Application US/10027632

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DB 6; Length 559;

64; Indels

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RESULT 13
JS-10-027-632-244811
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Publication No. US20030204075A9
                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-9
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                      PELICANT: Wang, David G.
ITLE OF INVENTION: Polymorphisms in the Human Genome
LLE REFERENCE: 108827.129
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WITLE OF INVENTION: Identification and Mapping of Single Nucleotide
WITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                         RRENT APPLICATION NUMBER: US/10/027,632
RRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/146,002 FILING DATE: 1999-08-09
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G DATE: 1999-11-23
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                                                              ON NUMBER: US 60/146,002
                                                                                                        ON NUMBER: US 60/156,358
                                                                                           1999-09-28
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51.9%; Pred. No. 6.3;
tive 0; Mismatches
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***FROTH: 79467
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US-10-027-632-244811
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Best Local Similarity
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TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71087/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT FILING DATE: 2002-08-15
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NUMBER OF SEQ ID NOS: 241
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PRIOR APPLICATION NUMBER: US 09/798,586
                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (13773)..(13370)
OTHER INFORMATION: "n" at positions 13273 to 13370
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (10089)..(10620)
OTHER INFORMATION: "n" at positions 10089 to 10620
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                               NAME/KEY: misc feature OCATION: (46579)..(46
                                                                                                                     NAME/KEY: misc_feature
LOCATION: (30751)..(30
                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (20762)..(20
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OTHER INFORMATION: "n" at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (5502)..(552
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INFORMATION: "n" at positoins 46759 to 46772 can be any base
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                                                                                                                                                                    ON: (20762)...(20781)
INFORMATION: "n" at positions 20762 to 20781 can be any base
                                                                                        ON: (30.751)..(30.916)
_INFORMATION: "n" at positions 30.751 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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                            (46772)
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Matches Query Match Best Local !

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**Local** 

SOFTWARE: FastS SEQ ID NO 244811

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (77382)..(77401)
; OTHER INFORMATION: "n" at positions 77372 to 77401 can be any base US-10-052-482-223
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Publication No. US20040110158A1
GENERAL INFORMATION:
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Best Local Similarity 56.4
Matches 57; Conservative
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                                                                                                                                                                   Matches
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TITLE OF INVENTION: MODULATION OF MITOCHONDRIAL RIBOSOMAL PROTEIN L13 EXPRESSION
FILE REFERENCE: RTS-0478
CURRENT APPLICATION NUMBER: US/10/317,273
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 159
                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: 11187, 11188, 11189, 11190,
LOCATION: 11196, 11197, 11198, 11199,
LOCATION: 11204, 11205, 11206, 11207,
LOCATION: 11212, 11213, 11214, 11215,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 11220
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 11121, 11122, 11123, 11124, LOCATION: 11130, 11131, 11132, 11133, LOCATION: 11138, 11139, 11140, 11141, LOCATION: 11146, 11147, 11148, 11149, DOTHER INFORMATION: n = A,T,C or G
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TYPE: DNA
ORGANISM: H. sapiens
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LOCATION: 11154, 11155, 11156, 11157,
LOCATION: 11163, 11164, 11165, 11166,
LOCATION: 11171, 11172, 11173, 11174,
LOCATION: 11179, 11180, 11181, 11182,
OTHER INFORMATION: n = A,T,C or G
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                         TCTTACTCATGCAACTTCCA 129
                                                                                                            TTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGGATACCTACTCCCAAACAATCCA 109
TCTTTCTCAGCAAACTTCTA 20134
                                                                                  TTTCTTTTTCTAAAACTGAAATTCCATGAAAAAAGAGAATATCAATTTTAAAAACTACCCA
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56.4%; Pred. No. 39;
tive 0; Mismatches
                                                                                                                                                             19.4%; Score 30.4; DB 7; Length 52001; 61.2%; Pred. No. 39; tive 0; Mismatches 31; Indels 0;
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, 11134, 11135, 11136, 1
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11169, 11170,
11177, 11178,
11185, 11186
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Search completed: March 6, 2006, 03:55:15 Job time : 226:751 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	March 6, 2006, 01:58:03 ; Search time 163.89 Seconds (without alignments) 2100.307 Million cell updates/sec
Title: Perfect score:	US-10-713-381-2_COPY_1155_1311 157
Sequence:	1 cgtgtcatctcacatggcatgcacatatgtttcctgaac 157
Scoring table: IDENTITY_NUC Gapop 10.0 ,	IDENTITY NUC Gapop 10.0 , Gapext 1.0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

14437070

7218535 seqs, 1096242582 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications NA New:\*

1: //cgn2\_6/ptodata/2/pubpna/US08 NEW\_PUB.seq:\*

2: //cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

PUB.seq:\* n2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq: \*
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n2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq: \*
n2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq: \*
n2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq: \*
gn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq2: \*
gn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq3: \*
gn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq3: \*
gn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq3: \* 6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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17.8	17.8	18.0	18.1	18.1	18.1	18.1	18.3	18.3	18.3	18.7	19.0	19.0	19.0	19.0	19.2	19.4	19.5	19.6	20.0	Query Match
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 Sequence 32050, A	Sequence 173193,	Sequence 724023,	Sequence 33980, A	Sequence 33977, A	Sequence 33976, A	Sequence 845392,	Sequence 47517, A	Sequence 47517, A	Sequence 805392,	Sequence 209, App	Sequence 12385, A	Sequence 285328,	Sequence 285327,	Sequence 285326,	Sequence 153052,	Sequence 13, Appl	Sequence 185, App	Sequence 778732,	Sequence 871704,	Description

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	ORGANISM: Homo sapiens				SOFTWARE: FastSEQ for Windows Version 4.0	NUMBER OF SEQ ID NOS: 957086	PRIOR FILING DATE: 2001-05-09	APPLICATION NUMBER: US 60/289,846	FILING DATE: 2001-01-16	APPLICATION NUMBER: US 60/261,766	FILING DATE: 2000-11-30	APPLICATION NUMBER: US 60/250,092	FILING DATE: 2000-11-20	APPLICATION NUMBER: US 60/252,147	FILING DATE: 2000-10-24	PRIOR APPLICATION NUMBER: US 60/243,096	CURRENT FILING DATE: 2001-08-08	CURRENT APPLICATION NUMBER: US/09/925,065A	FILE REFERENCE: 108827.135	••	INVENTION: Identification and Mapping of Single	APPLICANT: Wang, David G.	•••	Publication No. US20040181048A1	Sequence 871704, Application US/09925065A		
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																				TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome							
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Query Match  Best Local Similarity 60.2; Pred. No. 2.7;  Matches 50; Conservative 1; Mismatches  Qy 4 GTCATCTCACATGCATACTACATGCTTGTTCAL  Db 274 GGCCTCTTGCTTGAACGAGGCCCATGCTTGGTTTT  Qy 64 CCTTGCTTATTCTGAACGAGG 86	atch 20.0%; Score 31.4; DB cal Similarity 60.2%; Pred. No. 2.7; 50; Conservative 1; Mismatchers; 4 GTCATCTCACATGCATACTACATGCTTGTTCAAC,	RE	В	Ş	Вb	Ş	·	
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N_K " H	DB 6; ; 32; ; 32; ;AACGGTT	N	334 TCATGATAATTTTGAACAARGAG 356	64 CCTTGCCTATTCTGAACCAAGAG 86	274 GGCCTCTTGCTTGGAAGAGCCCATGCTTGGTTT	4 GTCATCTCACATGGCATACTACATGCTTGTTCF	hes 50; Conservative 1; Mismatches	y Match 20.0%; Score 31.4;
6; Length 56 32; Indels 32; Indels 3GTTCGTCTTGTTC 1					cerci	CATCG	0;	5,
Length 565; Indels 0; CGTCTTGTTCCATCG                 CTTCTGTCTCCCGTCT	o; carcg				TGAAAT	TCCAAG	Gaps	
Length 565; Indels 0; Gaps CGTCTTGTTCCATCGTCCAAG	0; Gaps 0; Gaps CATCGTCCAAG             CGTCTTGAAAT				333	63	0;	

US-09-925-065A-778732/c

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US-11-117-187-185
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; ORGANISM: Homo sapiens
US-09-925-065A-778732
                                               US-11-117-187-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 185, Application US/11117187 Publication No. US20050266560A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                         APPLICANT: COPENIAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 1090-03-18
NUMBER: 05 SEQ ID NOS: 212
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Huma
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
EQ ID NO 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: PREUSS, DAPHNE APPLICANT: COPENHAVER, GI
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NUMBER OF SEQ ID NOS: 957086
                                                           PEATURE:
NAME/KEY: modified base
LOCATION: (9960) . (21144
OTHER INFORMATION: N = 1
                                                                                                                                                     ORGANISM: Arabidopsis thaliana
                                                                                                                                                                            TYPE: DNA
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APPLICATION NUMBER: US 60/261,766
FILING DATE: 2001-01-16
APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 ATTATAAATGATAAATTTTTCTATACACATACAGTTTTTCTACCCATATTATCTTTCCTA 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
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larity 52.3%;
Conservative
  19.5%;
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; Pred. No. 4.3;
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Score 30.6;
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12;
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Length 64415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 153052, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/11121086
Publication No. US20050266459A1
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                                                          SOFTWARE: FastSEQ
SEQ ID NO 153052
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APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OP INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR PILICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                             FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
                                                                                                                                       PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/250,092 PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/252,147 PRIOR FILING DATE: 2000-11-20
                                                                                                  NUMBER OF SEQ ID NOS: 957086
                                                                                                                       PRIOR FILING DATE:
                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/261,766
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ORGANISM: Homo sapiens
                  TYPE: DNA
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                                         ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 CTCATGCAACTTCCATGCAAACACGCACATATGTTT 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
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                                       436
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                                                                               for Windows Version 4.0
                                                                                                                       2001-05-09
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Pred. No. 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 191797;
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                                                                                                                                                                                                                                                                                                                                                                                      Human Genome
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Score 30.2; DB 6; Pred. No. 6.1;

Length 436;

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RESULT 6
US-09-925-065A-285326
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; ORGANISM: Homo sapiens US-09-925-065A-285326
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Best Local Similarity 60.2%;
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                        CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                    APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR FILING DATE: 2000-10-24
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TLE OF INVENTION: Identification and Mapping of Single
TLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                             yence 285327, Application US/09925065A
lication No: US20040181048A1
FILING DATE: 2000-11-20
APPLICATION NUMBER: US 60/250,092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 TACCTGCACTRAAGTTAAATG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 AACACGCACATATGTTTCCTG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 TGTGTAGAAATTTAATACATACTTCCAAACAATCCAGAGTTTTGTAGCAACTTATACTCC 432
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Similarity 60.5%;
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                              CATION NUMBER: US 60/252,147 IG DATE: 2000-11-20
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Pred. No. 9;
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US-09-925-065A-12385

Sequence 12385, Appl Publication No. US20 GENERAL INFORMATION:

Application US/09925065A US20040181048A1

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US-09-925-065A-285328
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US-09-925-065A-285327
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NUMBER OF SEO ID NOS: 957086

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 285227
                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 285328
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Best Local
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 108827.135
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PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/261,766 FILING DATE: 2001-01-16
                                                                                 373
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                                      134 AACACGCACATATGTTTCCTG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 TACCTGCACTGAAGTTAAATG 453
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433 TÁCCTGCÁCTGÁAGTTAAATG
                                                                                                                          74 ТСТВААССААВАСБАТАССТАСТСССАААСААТССАТСТТАСТСАТВСААСТТССАТВСА 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/925,065A
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                                                                                                                                                                                         Similarity
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                                                                                 TGTGTAGAAATTTAATACATACTTCCAAACAATCCAGAGTTTTGTAGCAACTTATACTCC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                      ICATION NUMBER: US 60/289,846
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                                                                                                                                                                     Score 29.8; DB Pred. No. 9; 0; Mismatches
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Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                              DB 6; Length 617;
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RESULT 10
US-11-117-187-209/c
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; ORGANISM: Arabidopsis thaliana
US-11-117-187-209
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ARCD:309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 209, Appublication No.
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SEQ ID NO 12385
                                                                                                                                                                                                                                                                                                                        SEQ ID NO 209
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                                                                                                                                       Matches
                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 957086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                ENGTH: 611587
                                          270144 TCTCTCCTGCCAAGCGAATGGATTTGTCATGCATTTGTTGCTAACTGCCGACACAAGCTG 270085
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68 GCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTC 127
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                                                                                                                                       66;
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                                                                                     TCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTT 67
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                                                                                                                                                          18.7%;
                                                                                                                                   Score 29.4; DB 12;
Pred. No. 91;
0; Mismatches 61;
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Pred. No. 11;
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; ORGANISM: Homo sapiens
US-09-925-065A-805392
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CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2000-10-8-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-16
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                                         US-10-750-185-47517
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                                                                                                                           PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 475.7
SEQ ID NO 475.7
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Publication No. US20050260603A1
GENERAL INFORMATION:
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LENGTH: 544
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Query Match
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Best Local Similarity
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MMI GENOMICS, INC. APPLICANT: DENISE, Sue K. APPLICANT: KER, Richard APPLICANT: ROSENFELD, David
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                 ORGANISM: Bovine
                                                                                      LENGTH: 1370
TYPE: DNA
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  18.3%; Score 28.8;
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Pred. No. 1
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  DB 8;
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  Length 1370;
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US-09-925-065A-845392
JS-09-925-065A-845392, Application US/09925065A
Sequence 845392, Application US/09925065A
Publication No. US20040181048A1
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; ORGANISM: Bovine 19866880570548
US-10-750-623-47517
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SEQ ID NO 47517
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TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAILIO0-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
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                   PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION DATE: 2001-01-16
                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/925,065A
                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                          PPLICANT: Wang, David G.
ITIE OF INVENTION: Identification and Mapping of Single
ITIE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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les 57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            660 TIGITITCCTCATGCTTGCCGCTCCCATTCAGGGACTAGAAGCTGAAAACTCTGAAATTAT 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTT 150
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ICATION NUMBER: US 60/289,846
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HOLM, Tom
BATES, Stephen
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54.8%; Pred. No. 24
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US-09-925-065A-845392
                                                                                                                                                         Search completed: March 6, 2006, 10:32:51 Job time : 165.89 secs
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US-09-925-065A-33976
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US-09-925-065A-33976/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQ ID NO 33976
; LENGTH: 1691
; TYPE: DNA
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LENGTH: 628
TYPE: DNA
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GENERAL INFORMATION
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PRIOR PILING DATE: 2000-11-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION: Identification and Mapping of Single ITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/261,766
                                                                                                                                                                                                                                                                                                                               1191 TGGTGCTGGCCTCCAGATAGTGAGTTCTTGTAAGACTTGGTCATTTAAAAGTGTGCGGCT 1132
                                                                                                                                                                                                                                                1131 CCCCACTGCCCACTCTCTCTCTTGCTGCCTTTGCCATG 1090
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56; Conserv
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Pred. No. 34;
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Pred. No. 28
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(c) 1993 - 2006 Biocceleration Ltd.
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Title: Perfect score: Sequence:	
US-10-713-381-2_COPY_11/9_1408 30 1 catgcttgttcaaccgttcgtcttgttcca 30	

Searched:	Scoring table:
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Total of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	19.6	19.6	19.6	19.6	19.6	19.6	.20	20	20	20.2	20.4	22	24.2	. 30	30	30	30	30	30	Score
	65.3	65.3	65.3	65.3	65.3	65.3	66.7	66.7	66.7	67.3	68.0	73.3	80.7	100.0	100.0	100.0	100.0	100.0	100.0	Query Match Length
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2.	Acl37405 Rice stre	Ada72530 Rice gene		Rice	Ada72061 Rice gene	Acl35519 Rice stre		Acl34976 Rice stre		Aca44013 Prokaryot	Abz13819 Arabidops			Aah76333 Z. mays M	Aah76332 Z. mays M	Aax07409 Zea mays			2	Description

The invention provides a male tissue-preferred regulatory region (1) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (1) into a plant where the exogenous gene impacts male fertility of the plant and (1) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The

of,

A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

45	43	42	41	40	39	38	37	36	35	34	ယ	32	31	30	29	28	27	26	25	24	23	22	21	20	
18.8	18.8	18.8	18.8	18.8	18.8	18.8		18.8	18.8	19	19	19	19	19	19.	19	19	19	19.2	19.4	19.4	.19.4	19.4	19.6	
62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	. 7	٠	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3		. 7	64.7	64.7	64.7	65.3	
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## ALIGNMENTS

RESULT 1	以11
ij	AAH76335 standard; DNA; 30 BP.
ĕ	AAH76335;
H X	29-OCT-2001 (first entry)
ž	water wale tierne-professed regulatory region
XE	Antacory region
<b>2</b> 2	Ms45; male tissue; regulatory region; transcription; male tertility; hybrid seed; ds.
2 \$	
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X P	WO200160997-A2.
g g	23-AUG-2001.
P.	13-FEB-2001; 2001WO-US004527.
₩ Š	15-FEB-2000; 2000US-00504487.
PAX	(PION-) PIONEER HI-BRED INT INC.
PX	Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
뮻홌	WPI; 2001-514772/56.
X	5
14.	for initiating transcription of the MS45 gene useful
¥ ¥	mediating fertility in a male plant.
XX Sq	Claim 5; Page 47; 50pp; English.
C	erred regulatory
3 6	comprising nucleotide sequences essentiat for intracting transcripts
ດດ	provided that involves introducing an expression vector comprising a
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AAH761
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DT 29-C
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RESULT 3
AAX07408
ID AAX07408 standard; DNA; 1394 BP.
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Best Local :
                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence represents a DNA fragment -152 to -181 bases upstream the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
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                                                                                                                                                                      CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                                                                                                                                                                                                                                                                                                                                          255
                                                                                                                              CATGCTTGTTCAACCGTTCGTCTTGTTCCA
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                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                        BP; 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOX TW,
                                                                                                                                                                                                                                                                                                                                        A; 86 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INT INC
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                                                                                                                                                                                                                                 Score 30; DB Pred. No. 0.0); Mismatches
                                                                                                                                                                                                                                                                                                                                        39 G; 71 T; 0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB 5;
Pred. No. 0.0045;
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                                                                                                                                                                                                                                                                                    Length 255;
                                                                                                                                                                                                                                                                                                                                             Other;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolls and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M845; male; tissue-preferred; plant tissue; differentiated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX07408;
                                                                                                                                                                                               08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1394 BP; 411 A; 311 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 22-23; 39pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-1997;
                                                                                                                          Ms45; male; tissue-preferred; regulatory region; plant plant tissue; differentiated; hybrid seed; fertility;
                                                                                                                                                                    Zea mays Ms45 male tissue-preferred regulatory region.
                                                                                                                                                                                                                                                     AAX07409 standard; DNA; 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-1998;
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                                           30-DEC-1998
                                                                     WO9859061-A1
                                                                                                Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                        1179 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 1208
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                                                                                                                                                                                                                                                                                                                                                  CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                      ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory region; plant cells; maize; hybrid seed; fertility; ss
                                                                                                                                                                                                                                                                                                                                                                                           Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   231 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huffman GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                   441 T;
                                                                                                                                                                                                                                                                                                                                                                                           0.007;
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19-JUN-1998;

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RESULT 5
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Best Local
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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a
                                                                                                A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                        Claim 4; Page 46; 50pp;
                                                                                                                                                                                      Albertsen
                                                                                                                                                                                                                                           15-FEB-2000; 2000US-00504487
                                                                                                                                                                                                                                                                      13-FEB-2001; 2001WO-US004527.
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                                                                                                                                                                                                                                                                                                                               WO200160997-A2.
                                                                                                                                                                                                                                                                                                                                                          Zea mays

    mays Ms45 male tissue-preferred regulatory region encoding DNA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants
                                                                                                                                                                                                                 (PION-)
                                                                                                                                                                                                                                                                                                                                                                                      hybrid
                                                                                                                                                                                                                                                                                                                                                                                                 Ms45; male tissue;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 23-24; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-105628/09
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                                                                                                                                                                                                                                                                                                                                                                                    seed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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llarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid encoding a Ms45 male tissue-preferred regulatory region mediating plant fertility, especially hybrid seed production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                      Fox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 1394
                                                                                                                                                                                                                                                                                                                                                                                              regulatory region;
                                                                        English.
                                                                                                                                                                                   Garnaat CW,
                                                                                                                                                                                                                 INT INC
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Pred. No. 0.007;
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                                                                                                                                                                                                                                                                                                                                                                                              transcription; male fertility;
                                                                                                             comprising nucleotide sequences the MS45 gene useful for
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1179 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 1208

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                               Query Match
Best Local s
Matches 30
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                                                                                                           The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 matissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                       A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                     Sequence 1394 BP;
                                                                                                                                                                                                                                                               Claim 4; Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2001; 2001WO-US004527
                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-514772/56
                                                                                                                                                                                                                                                                                                                                                                                 Albertsen MC,
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    mays Ms45 male tissue-preferred regulatory region encoding DNA

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                                                                                                                                                                                                                                                                                                                                                                                                              (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ms45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  male tissue;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seed;
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                                             Similarity
CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                                                                                                                                                                                                                                                                                                 Fox TW,
                                                                                 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulatory region; transcription; male fertility;
                                                          100
                                             100.0%;
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100.0%; Pred. No. 0.00
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                                           Score 30;
Pred. No.
                              Mismatches
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                                             0.007;
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                              Indels
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expression of the
s also provided. The
encoding an Ms45 male
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                          Gaps
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                                                                                                                     the
1. The
male
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lung

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RESULT 8
ABQ75351/c
ID ABQ75351 standard; cDNA; 1304 BP
XX
AC ABQ75351;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human lung specific nucleic acid
XX
KW Human; lung; lung specific nucle
XX
KW LSP; cytostatic; gene therapy; v
KW squamous cell carcinoma; gene; s
XX
OS Homo sapiens.
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Best Local
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -38 to -195 bases upstream of the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M845; male tissue; regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z. mays Ms45 male tissue-preferred regulatory region fragment.
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                                                               Human; lung; lung specific nucleic acid; LSNA; lung specific protein;
LSP; cytostatic; gene therapy; vaccine; metastasis; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514772/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-2000; 2000US-00504487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mayв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hybrid seed;
                                                                                                           Human lung specific nucleic acid sequence SEQ ID NO:90.
                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide sequence
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                                                                                                                                                                                                                                                                               25
                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                               CATECTTCTTCAACCGTTCGTCTTTGTTC 53
                                                                                                                                                                                                                                                                                                           CATGCTTGTTCAACCGTTCGTCTTGTTCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MC.
                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    BP; 41 A; 50 C; 21 G; 46 T; 0 U; 0 Other;
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                                               ic; gene therapy; vaccine; metastasis;
carcinoma; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                      80.7%;
89.7%;
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                                                                                                                                                                                                                                                                                                                                                      Score 24.2;
Pred. No. 1.6
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                                                                                                                                                                                                                                                                                                                                           Mismatches
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising nucleotide sequences the MS45 gene useful for
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RESULT 9
ABZ13819
ID ABZ1
XX ABZ1
XX ARBZ1
XX ARBZ1
XX ARBZ1
XX ARBZ1
DT 21-J
XX ARBZ1
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XX ARBZ1
DT 21-J
XX ARBZ1
DT 21-J
PR 24-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an isolated lung specific nucleic acid (CC (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid CC sequences comprising 17 - 733 amino acids, given in ABP52873 to ABP52865; CC (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp), CC given in ABQ75262 to ABQ75376; (c) selectively hybridises to (a) or (b); CC or (d) has 60 % sequences identity to (a) or (b). LSNA and lung specific CC protein (LSP) sequences have cytostatic activity and can be used in gene CC therapy and vaccines. LSNAs and LSPs are useful for diagnosing and CC monitoring the presence and metastases of lung cancer in a patient. An CC antibody that specifically binds to an LSP can be used for determining CC with lung cancer, particularly by inducing an immune response against the CC lung cancer cell expressing the LSNAs or LSPs. In particular, these LSNAs CC and LSPs are useful for identifying, diagnosing, monitoring, staging, staging, CC imaging and treating lung cancer (e.g. squamous cell carcinoma) and non-cc cancerous disease states in lung
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Matches
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Best Local
                             24-AUG-2000;
26-JAN-2001;
22-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New lung specific nucleic acid useful in gene therapy or as vaccines treating lung cancer (e.g. squamous cell carcinoma) or non-cancerous diseases, as well as for diagnosing, monitoring or staging these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-2000; 2000US-0252054P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ13819;
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                                                                                                                                                                                                                                                                                                                                          Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana stress regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2003
                                                                                                                                  24-AUG-2001;
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                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGCTTGTTCAACCGTTCGTCTTGTTCCA
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                                                                                                                                                                                                                                                                                                                                          thaliana; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                     2000US-0227866P
2001US-0264647P
                                                                                                                                  2001WO-US026685
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206; 282pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,</u>
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Pred. No. 18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                       gene; stress; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sun Y,
                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1624.
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Market Statement

江下華八七章 11771

isolate candidate molecules for rational drug discovery programs.

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RESULT 10
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Best Local (
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Wall
                                                                                                                                                               21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0049299.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.
                                                                                                                                                                                                                                                                                           21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                             03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                     WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas putida.
WPI; 2003-029926/02
P-PSDB; ABU40143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prokaryotic essential gene #25670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that in methods of the invention. Note: The sequence data for this patent is methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                              (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1542 BP; 345 A; 382 C; 370 G; 445 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identifying a stress condition to which a cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 144; SEQ ID NO 1624; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SCRI ) SCRIPPS RES INST.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                              'nΉ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 CATGATTGTTCAACCAATCGTCGGTTTCCA 266
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                                                                                                                            ELITRA PHARM
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                                                           Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                           Malone
Carr (
                                                                                                                            INC.
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                                                           ર્તુ <sup>(</sup>
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                                                      Haselbeck R,
Yamamoto R,
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                                                      Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6;
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Sequence

2397 BP; 415 A; 825 C; 781 G; 376 T; 0 U; 0 Other;

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The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid (CC encoding a polypeptide whose expression is inhibited by the antisense cCC nucleic acid; (2) a host cell containing the vector; (3) an isolated CC entrisense nucleic acid; (4) an antibody capable of specifically binding CC proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for the gene product or that has an activity against a biological pathway of crequired for proliferation, or that inhibits cellular proliferation of the treative for cellular proliferation of the pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiocic; (10) profiling a compound to a compound acts; (9) manufacturing an antibiocic; (10) profiling a compound to a compound to a compound the control of the strains is present in a culture or collection of the strains; is present in a culture or collection of contentifying proteins or screening for homologous nucleic acids required contentifying proteins or screening for homologous nucleic acids required contentifying proteins or for screening homologous nucleic acids required contentify and the content content of the co
                                                                                drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; SEQ ID NO 31883; 1766pp; English.
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RESULT 11 ACL37526 밁 Ś Matches Query Match ss; abiotic stress tolerance; transgenic plant; plant; cereal; agriculture. Rice stress-regulated promoter SEQ ID NO:16089 02-JUN-2005 ACL37526; ACL37526 standard; cDNA; Local 516 CATGCTGGTACAACCGTTCGGCTTG 540 1 CATGCTTGTTCAACCGTTCGTCTTG 25 22; Similarity 88.( 22; Conservative 67.3%; 2000 ç Pred. No. 1 В₽ Mismatches .2e+02; DΒ 8 3; Indels Length 2397; 0; Gaps

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to

22-JUN-2001; 2001US-0300112P 24-AUG-2001; 2001US-0314662P 26-SEP-2001; 2001US-0325277P 21-NOV-2001; 2001US-0332132P

21-JUN-2002; 2002WO-US019668

30-JAN-2003

Oryza sativa. WO2003008540-A2

WPI; 2003-248011/24

(SYGN)

SYNGENTA PARTICIPATIONS

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Briggs SP, T, Provart

Cooper N, Ric

per B, Ricke

'n

Glazebrook J, ), zhu T;

Goff

SA,

Katagiri

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ACL34976
ACL34976
ACL3
XX
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AC ACL3
AC ACL3
XX
C ACL3
AC ACL3
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Rice
XX
KW 88;
KW 88;
KW agr:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, samotic stress or any of their combinations. The present sequence is the company of their combinations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2000 BP;
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                                                      WPI;
                                                                                                                                                                                                                                        22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0332277P.
21-NOV-2001; 2001US-0332132P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agriculture
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     New
                                                                                                        Moughamer
                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2003
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                                                                                                                                                                                    (SYGN )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abiotic stress tolerance; transgenic plant; plant; cereal;
  stress-responsive nucleic acid, useful
                                                      2003-248011/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                    SYNGENTA
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                                                                                                     Briggs SP,
T, Provart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                    PARTICIPATIONS
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82.1%;
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                                                                                                          Cooper B,
N, Ricke
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Pred. No.
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                                                                                                                                                                                       ĀG
                                                                                                          Glazebrook J,
D, Zhu T;
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  for altering
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                                                                                                                                   Goff
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     the
                                                                                                                                   Katagiri
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Budworth

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Moughamer T,

Brigge

SP,

Cooper

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Glazebrook

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RESULT 13
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, sants to an abiotic stress, such as cold stress, salts stress, osmotic stress or any of their combinations. The present sequence is the second of the present sequence is the second of the present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet, maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant; nutrition; apical dominance; dwarfism; early flowering; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is used in the exemplification of the invention
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                                                                                                                                                                (BRIG/)
(COOP/)
(GLAZ/)
(GOFF/)
(KATA/)
                                                                                                                                                                                                                                                                                                    (MOUG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antifungal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ40785
                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2001;
26-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota
                                                                                                          (PROV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2002;
                                                                                                                                         KREP/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1179
                                    HEPS J.
PROVART N.
RICKE D.
ZHU T.
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                                                                                                                                                                                                                                                                                                 BUDWORTH P.
                                                                                                                                                                                                                                                    BRIGGS S P. COOPER B.
                                                                                                                                                                   GOFF S A.
KATAGIRI F
                                                                                                                                                                                                                        GLAZEBROOK J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; cDNA; 2000 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000 BP; 552 A; 438 C; 444 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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82.1%;
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Pred. No. 1.4e
0; Mismatches
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Kreps J,

Provart N,

Ricke

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And Market

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RESULT 14
ACL35519
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CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential

CC or constitutive transcription of an operatively linked nucleic acid

CC segment. The invention also relates to a method for augmenting a plant

CC genome and a method of identifying a gene, where its expression is

CC genome and a method of identifying a gene, where its expression is

CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive

CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,

CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

CC sorghum, rice or wheat. The polynucleotides and the polypeptides they

CC sorghum, rice or wheat the polynucleotides and the polypeptides they

CC sorghum, rice or wheat the polynucleotides and the polypeptides they

CC sorghum, rice or wheat to produce large quantities of foil or

CC sorghum, rice or wheat to produce large quantities or fungi, and to

CC proteins, to incur resistance to insecticides, viruses or fungi, and to

CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants

CC patent stress tolerance (e.g. salt, cold or drought) to ensure the plants

CC early flowering or altered metabolic pathways. This sequence are represents a

CC plant nucleic acid of the invention. Note: The sequence data for this

CC plant nucleic acid of the invention at sequence data for this

CC plant nucleic acid of the invention at sequence data for this

CC plant nucleic acid of the printed specification but was obtained in

CC patent did not form part of the printed specification but was obtained in
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Best Local
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                                                                                                                               22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0325277P.
21-NOV-2001; 2001US-0332132P.
                               Kreps J, Briggs SP,
Moughamer T, Provart
                                                                                                                                                                                                                                                                                                                                                                                                                  ss; abiotic stress tolerance; transgenic plant; plant; cereal;
                                                                                                                                                                                                                                  21-JUN-2002; 2002WO-US019668
                                                                                                                                                                                                                                                                                                                           WO2003008540-A2
                                                                                                                                                                                                                                                                                                                                                                                                           agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice stress-regulated promoter SEQ ID NO:14082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-2005
                                                                                         (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACL35519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 26; SEQ ID NO 1785; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1179
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New stress-responsive nucleic acid, useful for altering the responsiveness of a plant, e.g. cereal, to an abiotic stress such stress, salt stress or osmotic stress.
                                                                                                                      as
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Claim 48; SEQ ID NO 14082; 89pp; English.

The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the tresponsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmotic stress or any of their combinations. The present sequence is used in the exemplification of the invention

Sequence 1735 BP; 502 A; 368 C; 279 G; 581 T; 0 U; 5 Other;

뮍 Ś Matches Query Match 394 v 22; Similarity CTTGTTCAACCGTTCGTCTTGTTCCA 30 CATGITTAACCGITCGICTTATICAA 419 Conservative 65.3%; Score 19.6; D Pred. No. 2e+0 0; Mismatches 0, 6; DB 11; 2e+02; 4 Indels Length 1735; ۰, Gaps 0

RESULT 15 ADA72061 ADA72061; ADA72061 standard; DNA; 2000 쁌

Rice gene, SEQ ID 5386. (first entry)

20-NOV-2003

gene; Plant; bacterial infection; fungal infection; viral infection; rice; dв.

Oryza sativa

WO2003000898-A1

03-JAN-2003.

22-JUN-2001; 2001WO-IB001105

22-JUN-2001; 2001WO-IB001105.

(SYGN ) SYNGENTA PARTICIPATIONS ĀG

Chang H, Chen W, Katagiri F, Quan Cooper B, S, Tao Y, Glazebrook J, () Whitham S, Xie Goff ie Z, SA, Zhu T, Hou

Zou

Ġ.

Identifying at least pathogenic infection bacterial, fungal or gene expression. one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant 6 6

27; SEQ ID NO 5386; 899pp; English

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered ij

WPI; 2003-248011/24

the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

Sequence 2000 BP; 605 A; 377 C; 326 G; 690 T; 0 U; 2 Other;

8888888888Ś Query Match 65.3%; Score 19.6; DB 8; Length 20 Best Local Similarity 84.6%; Pred. No. 2.1e+02; Matches 22; Conservative 0; Mismatches 4; Indels 5 CTTGTTCAACCGTTCGTCTTGTTCCA 30 Length 2000; 0; Gaps

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Search completed: March 5, 2006, 18:11:42 Job time: 19.9642 secs

974 CATGITTAACCGITCGICTTATICAA 999

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Page 8

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BB636596 BB936596
BG354114 00661 Lea
BP561510 BP561510
AV439701 AV439701
AV825937 AV825937
CA230882 SCJFFL3C0
CV153842 Eucinetus
CW788317 SP Ba004
BH876120 hr29D04.9
CLF83422 OB Ba004
BH876120 hr29D04.9
CLF83422 OB Ba004
AQ453944 HS 5165.B
CV153844 Eucinetus
AQ260121 CITBI-E1-
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CD836126 BM55.059M
CD836328 BM45.0481
BH480110 BOGHY44TR
BZ684539 BM50031TD
B10570 T15J6-T7.TA
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Title: Perfect score: Sequence:

US-10-713-381-2\_COPY\_1179\_1208 . 30
1 catgcttgttcaaccgttcgtcttgttcca 30

March 5, 2006, 18:11:59; Search time 141.632 Seconds (without alignments) 9910.279 Million cell updates/sec

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OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration

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# ALIGNMENTS

Query Match Best Local Matches 3	ORIGIN	FEATURES source	_	. 3	Z . U
Watch 100.0%; Score 30; DB 9; Local Similarity 100.0%; Pred. No. 0.024; nes 30; Conservative 0; Mismatches	/mol_type=genumic ban /strain=MSJ /strain=MSJ /strain=MSJ /db_xref="taxon:4577" /clone="TextMan0554D15" /clone=lib="ZM_0.7_1.5_KB" /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 methylation filtered genomic DNA library"	Tal: 301-838-5843 Fax: 301-838-0208 Email: whitelawatigr.org Seq primer: TF Class: methylation filtered. Location/Qualifiers 1.687 /organism="Zea mays" /mol type="genomic DNA"	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utt Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002) Other GSS: GCWDQ20TM Contact: Cathy Whitelaw TIGR 7712 Medical Center Drive, Rockville, MD 20850,	CC556393.1 GI:32060231 CC556393.1 GI:32060231 GSS. Zea mays Zea mays Zea mays Zea mays Zea mays Zea mays Andropophyta; Embryophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Eukaryota; Viridiplantae; Freptophyta; Eukaryota; Viridiplantae; Poolee; Pool	CC656939 DNA OCMD020TV ZM 0.7 1.5 KB Zea mays genomic
9; Length 687; 4; 0; Indels 0; Gaps 0;	1: HincII; 0.7-1.5 kb DNA library"		mD 20850, USA	ਨੂੰ ਨੂੰ	A linear GSS 19-JUN-2003 nic clone ZMMBMa0554D15,

Result No.

Score

Length

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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CC656939 OGMDQ20TV
CC252912 OGMDQ20TW
CC256931 OGMDQ20TM
CC444575 fsbb001f1
CG70047 ZMMBe01f1
CG70047 ZMMBe017
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BU030489 OHJ7N19.y
BU030489 OHJ7N19.3
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1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA

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Other GSSs: OG1AG08TH
Contact: Cathy Whitelaw
          1 (bases 1 to 963)

WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,

Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,

Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics

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4041 Forest Park Ave, 9
Tel: 314 615 6979
Fax: 314 615 5975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                 Email: jbedell@oriongenomics.com
plate: fsbb001f170 row: m colu
Seq primer: k Reverse
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Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 296)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 301-838-0208
Email: whitelaw@tigr.org
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9712 Medical Center Drive,
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                                                                                                                                                                                         High quality sequence stop: 296.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         Sorghum genome sequencing by methylation filtration PLOS Biol. 3 (1), e13 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CW445575.1
                                                                                                                                                                                                                                                                                                                                                                                     Contact: Bedell JA
                                                                                                                                                                                                                                   Class: methylation filtered
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/clone=1b="ZM 0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
prepared from purified nuclei was randomly sheared,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:4577"
                                         /clone_lib="Sorghum methylation filtered library (LibID: 104)"
                                                                             /db_xref="taxon:4558"
/clone="fsbb001f170m16"
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Pred. No.
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Y (LibID: 104)
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RESULT 6
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                                                                                              DEFINITION
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Best Local S
Matches 24
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           BU035739
QHJ7N19.yg.abl QH EFGHJ :
clone QHJ7N19, mENA seque
BU035739
BU035739.1 GI:22471259
EST
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Class: BAC ends
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Zea mays
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ZMMBBC0174H15f ZMMBBC (ECORI) Zea mays genomic clone
5', genomic survey sequence.
CG700474
CG700474.1 GI:37688275
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bharti, A.K.,
Zohovetz, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                      CATGCTTGTTCAACCGTTCGTCTTGTT
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el: 732 445 3801
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                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. coli DH10B"
/clome_lib="ZMMBBc (BcoRI)"
/note="Vector: pTARBAC2:1; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence start: 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                            74.0%;
88.9%;
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QH_EFGHJ sunflower RHA280 Helianthus
mRNA sequence.
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Pred No. 60;
0; Mismatches
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Pred. No. 0.3;
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EMMBBc0174H15
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BU030489/c
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                                       Helianthus annuus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; Campanulids; Asterales; Asteraceae; Asteroideae;

Heliantheae; Helianthus.
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QHJ15120,yg.abl QH ERGHJ sunflower RHA280 Helianthus
clone QHJ15120, mRNA sequence.
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                                                                                                                                                               Helianthus annuus (common sunflower)
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Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
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Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belonge to contig QH_CA_Contig3046, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                    (bases 1 to 626)
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te: QHJ7 row: N column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="0H_EFGHJ sunflower RHA280"
/note="Vector: pBrCNNASfiAB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. CDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TNG_IISSUE=flowers environmental stress
TNG_IISSUE=flowers sunflower RHA280
TNG_ISSUE=CGĀATGCGGG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Helianthus annuus"
|mol type="mRNA"
|/cultivar="RHA280"
|/db xref="taxon:4232"
|clone="QHJ7N19"
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88.5%;
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R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lavelle,D., Chevalier,P., Ziegle,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21.2;
Pred. No. 1.
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OX1_54_E01.g1_A002 Oxidatively-stressed leaves and roots Sorghum

bicolor cDNA clone OX1_54_E01_A002 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig3046, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome Project
                     Other_ESTs: OX1_54_E01.b1_A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                           Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C., Sun,F., Sullivan,R., Lim,S., Eastman,A. and Pratt,L.H. An EST database from Sorghum: oxidatively stressed leaves and roots
                                                                                                                                                                                                                                                                                                                                                                                                           Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://compgenomics.ucdavis.edu,
                                                                                                                                                                                                        Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CN137013.1 GI:45970259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CN137013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCTTGTTCAACCGTTCGTCTTGTT 27
                                                                                                                                                                                                                                                                                                             (bases 1 to 792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://gpdb.ucdavis.edu/TAG_TISSUE=flowers environmental stress
TAG_LIB=CH_EFGHJ sunflower RHAZ80
TAG_SEQ=CGAATGCGGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="QH_EFGHJ sunflower RHA280"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 11 different sources of RNA from a single genotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/clone="QHJ15I20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cultivar="RHA280"
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88.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21.2; DB 5;
Pred. No. 1.9e+02;
0; Mismatches 3;
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문 S

Trace considered overall poor quality

www-bio.llnl.gov/bbrp/image/image.html

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REFERENCE
AUTHORS
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SOURCE
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VERSION
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AA811551/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA811551 154 bp mRNA linear EST 19-FEB-1998 oa99e03.81 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320412 3' similar to SW:COPE_BOVIN Q28104 COATOMER EPSILON SUBUNIT ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., I
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.
1 (bases 1 to 154)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCTCCAACCGTTCGTCTTCTTCCA 42
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/(lab_host="DH10B-TI phage-resistant E. coli"
/(lone_lib="Oxidatively-stressed leaves and roots"
/(clone_lib="Oxidatively-stressed leaves and roots"
/(clone_lib="Oxidatively-stressed leaves and roots"
/(note="Organ: Leaf and Root; Vector: pWE188-FL3; Site_l:
/(note="Organ: Leaf and Root; Vector: pWE188-FL3; Site_l:
/(note="Organ: Leaf and Root; Vector: pWE188-FL3; Site_l:
//(note="Organ: Leaf and Root; Vector: pVE188-FL3; Site_l:
//(note="Organ: Leaf and Root; Vector: Leaves and roots were misted with hydrogen peroxide to 0.003% and leaves were misted with 10 uM methyl viologen. Leaves and roots were harvested at 3, 12 and 27 hr after treatment and all tissue pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME188-FL3 vector (5-prime DraIII site is CACTGTGTG, Vector: the own of the pwenty of the p
                                                                                                                                                                       Ph.D.
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/cultivar="BTx623"
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88.5%;
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Pred. No. 1.9e+02
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                                                  Sequencing Center
                                                                                                                                                                                                                                                                                                David Allman,
                                                                                                                                                                                                             M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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CR192459/c
LOCUS
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Best Local (
                                                                                                                                                                                                                                                                       TITLE
JOURNAL
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Best Local Similarity
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                                                     N
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                                                                                   24;
                                                                                                                                                                                                                                                 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CR192459 351 bp DNA Reverse strand read from insert in 5'HPR chromosome engineering clone MHPN146a06, CR192459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                                                                                                                                                                                                                                                                                           Adams, D. J., Biggs, P. J., Cox, A. V., Davies, R. M., Jonkers, J., Smith, J., Plumb, R. W., Taylor, R.G., Rogers, J. and Bradley, A.
                                                                                                                                                                                                                                                                                                                                                                                                 CR192459.1 GI:49971308
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 1232 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amerst
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Murrognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CR192459
                                                                                               Similarity
                                           ATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                         ATGCTGGTCCAGCCGTTCGTGATGTTCCA 279
                                                                                                                                                                                                                                                                                                                                            (bases 1 to 351)
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN146806"
/clone_lib="MHPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                          location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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82.8%;
                                                                                            70.0%;
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                                                                                Score 21; DB 11;
Pred. No. 2.1e+02;
0; Mismatches 5
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Pred. No. 1.8e+02;
0; Mismatches 5;
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5'HPRT insertion targeting and
46a06, genomic survey sequence.
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                                                                                                           Length 351;
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Nishijima,I., Yu,Y.,
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2 ATGCTTGTTCAACCGTTCGTCTTGTTCCA 30

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CR233964/c
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                                                                                                                                                                                                                                      Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi, Muroidea; Muridae; Murinae; Mus
1 (bases 1 to 599)
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Mus musculus (house mouse)
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Uonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y Rogers, J. and Bradley, A.
                         Similarity
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
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      Conservative
                                                                                                   /organism="Mus musculus"
/mol type="genomic DNA"
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/clone="MHPN144h08"
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/mol_type="genomic DNA"
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82.8%;
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                         Score 21;
Pred. No.
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Pred. No. 2.2e+02;
0; Mismatches 5
      Mismatches
                         2.3e+02;
                                         Length 599;
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                                                                                                                                                                                                                               Aedes aegypti (yellow fever mosquito)
Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryg
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Culicinae; Culicini; Aedes; Stegomyia.

1 (bases 1 to 832)
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
Unpublished (2003)
Other GSSS: NDL.2114.SP6
Contact: Brendan Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      832 bp DNA linear GSS
NDL.2I14.T7 Notre Dame Liverpool Aedes aegypti genomic
NotreDame Liverpool-2I14, genomic survey sequence.
CC848693
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Reverse strand read from insert in 5'HPRT insertion targeting and
chromosome engineering clone MHPN234h03, genomic survey sequence.
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24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 769)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y
Rogers, J. and Bradley, A.
Direct Submission
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                                                                           Email: enta@tigr.org
Library was provided
Seq primer: T7
                                                                                                                                 Tel: 301-838-3543
Fax: 301-838-0208
                                                                                                                                                                        9712 Medical Center Drive,
                                                                                                                                                                                                              Department of Eukaryotic Genomics
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                                                        Class: BAC ends
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nilarity 82.8%;
Conservative
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/mol_type="genomic DNA"
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/clone="MHPN234h03"
/clone_lib="MHPN"
/organism="Aedes aegypti"
                    Location/Qualifiers
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Pred. No. 2.3e+02;
0; Mismatches 5
                                                                                             David Severson
                                                                                                                                                                          Rockville,
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242 ATCCTTGTTCAACCATTTGTCTTGATTCA
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Library was provided l
Seq primer: T7
Class: BAC ends.
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1 (bases 1 to 835)

Loftus, B., Shetty, J., Knudson, D. and Severson, D.

BAC end sequencing of Aedes aegypti
Unpublished (2003)
Other GSSs: NDL. 2113.SP6
Contact: Brendan Loftus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301-838-3543
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
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                       ATGCTTGTTCAACCGTTCGTCTTGTTCCA
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/db xref="taxon:7159"
/clone="NotreDame Liverpool"
/clone lib="Notre Dame Liverpool"
/clone lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched Li larvae by David Severson at the University of Notre Dame and
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/db_xref="taxon:7159"
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3ndopterygota; Diptera; Nematocera; Culicoidea;
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1: /cgn2 6/ptodata/1.

2: /cgn2 6/ptodata/1.

3: /cgn2 6/ptodata/1.

4: /cgn2 6/ptodata/1.

5: /cgn2 6/ptodata/1.

5: /cgn2 6/ptodata/1.

6: /cgn2 6/ptodata/1.

7: /cgn2 6/ptodata/1.

8: /cgn2 6/ptodata/1.

9: /cgn2 6/ptodata/1.
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Match Length
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgnn_6/ptodata/1/ina/H_COMB.seq:*
/cgnn_6/ptodata/1/ina/PCTUS COMB.seq:*
/cgnn_6/ptodata/1/ina/PP_COMB.seq:*
/cgnn_6/ptodata/1/ina/RE_COMB.seq:*
/cgnn_6/ptodata/1/ina/RE_COMB.seq:*
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US-08-880-499-1
US-08-980-499-2
US-07-937-609-15
US-08-029-170-15
US-09-49-016-16262
US-09-949-016-1438
US-09-949-016-13180
US-09-949-016-767-13492
US-09-949-016-767-13492
US-09-949-016-200253
US-09-956-1718-1190
US-08-781-986-1190
US-08-781-986-1190
US-09-921-992-2
US-09-921-992-3
US-09-921-932-3
US-09-921-932-3
US-09-921-932-3
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Sequence 2, Appli
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
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. 17.4	17.4	17.4	17.4	17.8	17.8	17.8	17.8		17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
11034, A	820, App	178197,	169, App	17504, A	15779, A	13614, A	17490, A	12574, A	13439, A	9, Appli	16645, A	12327, A	<ol> <li>Appli</li> </ol>	193, App	174, App	204030,	204029,	142937,	17275, A	1993, Ap

### ALIGNMENTS

1, Application US/08880499 5. 6037523

; MOLECULE TYPE: DNA (genomic) US-08-880-499-1	
; STRANDEDNESS: single : ; TOPOLOGY: linear	
nuclei	
; LENGTH: 1394 base pairs	
FO	
; TELEFAX: (515) 248-4844	
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TRATION NUMBER: 32	
NAME: Sweeney Patricia A.	
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ON: 800	
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; APPLICATION NUMBER: US/08/880,499	
; SOFTWARE: PatentIn Release #1.0, Version #1.30	
; OPERATING SYSTEM: PC-DOS/MS-DOS	
; COMPUTER: IBM PC compatible	
; ZIP: 50131	
; COUNTRY: USA	
; STATE: IOWA	
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Box 1000	
arwin Building, 7100 N.W. 62nd Av	
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.	
Š	
R OF SEQUENCES: 2	
OF INVENTION: AND METHOD OF USING SAME	
NVENTION: MALE	
: Kendall,	
Huffman, Gary	
Carl,	
Fox, Tim W.	
; APPLICANT: Albertson, Marc C.	
; Patent No. 6037523	
, מפקעפווכם ב, אטטיבוכמניסוו סט/ ססססטיביי	

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7, Appli 7, Appli 200252, 200253, 1190, Ap 1190, Ap 1190, Ap 1, Appli 2, Appli 2, Appli 1, 1, 3, Appli 1, 38, Ap

Query Match

100.0%; Score 30;

DB 3; Length 1394;

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                                                                                                   US-07-937-609-15; Sequence 15, Application US/07937609; Patent No. 5319073;
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US-08-880-499-2
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                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                        US-08-880-499-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08880499 Patent No. 6037523
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                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                  Query Match
         GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: CONCURRENT
CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
STREET:
CITY: J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1394 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 50131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O STREET: Box 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1179 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 1208
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                                                                                                                                                                                                                                                           1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                                                                                                                                        CATGCTTCTTCAACCGTTCGTCTTGTTCCA 1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                             100.0%; Score 30; DB 3; ilarity 100.0%; Pred. No. 0.0012; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fox, Tim W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Albertson,
                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                              single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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; Mismatches 0;
                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                    Length 1394;
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Query Match
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US-08-029-170-15
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2243 has Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 436
PRIOR APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
PRIOR APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 40399/166 NIHD
TELEPAN/UNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAN: (703)838-4109
                                                                                                                                                                                                                                           Sequence 15, Application US/08029170 Patent No. 6169173
                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: WANK, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 1:
MOLECULE TYPE:
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                     APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1800 Lies
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                   CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19920902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                     ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22313-0299
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                                                                                                                                                                                                                                                                                                                                                                                   1 CATGCTTGTTCAACCGTTCGTCTTGTTCC 29
                                                                  VA
                                                                                                                                                                                                                                                                                                                                                   CCTGCTTGCTCAACTCTACGTCTTGTTTC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rat brain CCKB receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2243 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                     64.7%;
79.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15:
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19.4; D
Pred. No. 55;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                       Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                        9
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US-08-029-170-15
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                   ent No. 6/v....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
07/937,609
                                              ZIP: 22313-0299
MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: rat brain CCKB receptor
                                                                                                                                                                              DRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFERENCE/DOCKET NUMBER: 40 ECOMMUNICATION INFORMATION
                                                                                                                                                                                        SPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ION FOR SEQ ID NO:
CE CHARACTERISTICS
                                                                                                                                                  Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEIC ACIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                               CCTGCTTGCTCAACTCTACGTCTTGTTTC 33
                                                                                                                                                                                                                                                                                          Application US/09443745
                                                                                                                                                        3: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICATION DATA:
ION NUMBER: US 07/861,769
ATE: 01-APR-1992
                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TE: 02-SEP-1992
CATION DATA:
CON NUMBER: US 07/928,033
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136..1494
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YSTEM: PC-DOS/MS-DOS
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OMBER: US 07/831,248
07-FEB-1992
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                DATA:
                                                                                                                                                                                                                  CLONING AND FUNCTIONAL EXPRESSION CHOLECYSTOKININ RECEPTOR-ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                   64.7%;
79.3%;
                               Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40399/166 NIHD
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.4;
Pred. No. 55
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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LOCATION: 136
US-09-443-745-15
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Best Local Simi
Matches 23;
 Query Match
                           ORGANISM: Human
-09-949-016-16262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: rat brain CCKB receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFERENCE/DOCKET NUMBER: 4(
ECOMMUNICATION INFORMATION
                                                                        45571
                                                                                                                                                                                                                                                                                                                                                                                                                              1 CATGCTTGTTCAACCGTTCGTCTTGTTCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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CONTINUER: US 07/831,248
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CATION DATA: US 07/928,033
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N NUMBER: US 07/861,769
E: 01-APR-1992
                                                                                                                                                                                                                                                                                                                               Application US/09949016
                                                                                                                                                                                                                            ON NUMBER: US/09/949,016
                                                                                                 for Windows Version 4.0
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                                                                                                                                                                                                                2000-04-1
 63.3%; Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.7%; Score 19.4; 79.3%; Pred. No. 59
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                                                                                                                                                                                                60/241,755
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 DB 3;
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Length 45571;
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OF DETECTION AND USES THEREOF
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Pred. No. 1.4e+02;

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US-09-949-016-1438/c
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                                                                             US-09-949-016-1438
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Matches 22; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09368590 Patent No. 6187563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                  SEQ ID NO 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1438, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 101918-200 (OCR-941)
CURRENT APPLICATION NUMBER: US/09/368,590
CURRENT FILLING DATE: 1999-08-04
EARLIER APPLICATION NUMBER: 60/095,657
EARLIER FILING DATE: 1998-08-07
NUMBER OF THE STATE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Solimena, Michele
                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                             LENGTH: 8756
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: (2266)...(2268)
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LOCATION: (1021)...(1023)
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LOCATION: (1)...(6879)
NAME/KEY: unsure
LOCATION: (100)...(102)
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Pred. No. 1
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1.3e+02;
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Length 8756;
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Query Match

62.78;

Score 18.8;

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PRIOR APPLICATION NUMBER: 60/237,768

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RESULT 9
US-08-961-527-132
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                                                                                                                                                                                     RESULT 10
US-09-949-016-13180/c
                                                                                                                                     Sequence 13180, Application US/09949016 Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATE

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 109-8504

TOTERHONE: (301) 309-8504
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Best Local (
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VE.
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        Local
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23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                          62.7%;
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0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                            Score 18.8; DB 3; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                            Mismatches
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS:

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RESULT 12
US-09-270-767-13492/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Drosophila melanogaster US-09-270-767-29480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: (1) ... (112874)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-13180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patent
SEQ ID NO 29480
LENGTH: 549
                                                                                                                                     SEQ ID NO 13492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBEA
SOFTWARE: Fab
SEQ ID NO 13180
                                                                                                                                                                                                                                                                                                     Sequence 13492
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                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE; File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
NUMBER OF SEQ ID NOS: 62517
                                                                       09-270-767-13492
                                                                                                                                                    SOFTWARE: Patentin Ver.
                                                                                   ORGANISM: Drosophila melanogaster
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                     Local
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E OF INVENTION: Nucleic acids and proteins
REFERENCE: File Reference: 7326-094
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l Similarity 76.7%;
23; Conservative
                     Similarity
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21; Conservative
       Conservative
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               62.0%;
84.0%;
Score 18.6; DB 3
Pred. No. 1.1e+02
0; Mismatches
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Pred. No. 9
                 .1e+02;
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                                Length 1120;
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US-09-573-080A-7/c
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US-09-248-796A-3293
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Patent No. 6828097
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                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
DATABASE ENTRY DATE: 1996-01-26
                                                                                                                                 TITLE: Prototypic sequences for 
JOURNAL: Journal of Molecular
                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: repeat region
LOCATION: (1)..(2710)
                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/096,409
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                                                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: n i
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                                   ACCESSION NUMBER: Database for repetitive elements (repbase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROGAN, PETER
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                                                                                                                                                                    J; Walichiewicz,
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78.6%;
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                                                                                                                              Evolution
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Pred. No. 1.4e+02;
0; Mismatches 6;
                                                                                                                                              J; Milosavljevic, A
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-33
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR PILING 
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US-09-949-016-200252/c
; Sequence 200252, Application US/09949016
; Patent No. 6812339
; Patent No. 6812339
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Search completed: March Job time: 8.38752 secs
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.0%; Score 18; DB 3; Length 601; Best Local Similarity 80.8%; Pred. No. 1.8e+02; Matches 21; Conservative 0; Mismatches 5; Indels
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Title:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: /cgn2 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*
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Match Length
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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622 4
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4 8 US-10-713-381-2
8 8 US-10-713-381-2
9 8 US-10-011-879-903-6815
90 8 US-10-010-1676
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5 10 US-11-63-391-5
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6 US-09-925-065A-863989
4 4 US-09-925-065A-863989
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7 US-10-4425-513-5
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Sequence 4, Appli
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	Sequence 2535, Ap	Sequence 37788; A	Sequence 9220, Ap	Sequence 2217, Ap	Sequence 40048, A		•	22639	7281,	Sequence 971, App	183,	381,	971,		Sequence 279, App	Sequence 953397,	Sequence 936360,		47247		Sequence 729, App

# ALIGNMENTS

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NVENTION: MALE T	APPLICANT: KAKNAAL, CAKL W. APPLICANT: HUFFMAN, GARY APPLICANT: KENDALL, TIMMY L.	FOX, TIMOTHY W	; GENERAL INFORMATION:	 ; Sequence 9, Application US/10713381	RESULT 2 US-10-713-381-9	Db 1 CATGCTTCATCCATCGTCTTCCCA 30	Oy 1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30	Query Match 100.0%; Score 30; DB 8; Length 30; Best Local Similarity 100.0%; Pred. No. 0.008; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	, ORGANISM: Zea mays US-10-713-381-4	; LENGTH: 30 ; TYPE: DNA	; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 4	; PRIOR APPLICATION NUMBER: 08/880,499	CURRENT FILING DATE: 2003-11-14	PERENCE: 578R	; TITLE OF INVENTION: WHIB ILSSUS-FREEERRED REGULATORY REGION AND METHOD OF ; TITLE OF INVENTION: USING SAME	CANT: KENDALL, TIMMY L.	APPLICANT: GRAVANI GARY	: FOX, TIMOTHY W	; APPLICANT: ALBERTSEN, MARC C.	PUBLICATION NO. US20040221331A1  CENERAL THEORYTHAN	; Sequence 4, Application US/10713381	US-10-713-381-4	RESULT 1

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FILE REFERENCE: 578R

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CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-9
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SEQ ID NO 1
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Best Local Similarity
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Publication No. US20040221331A1
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APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: HUFFMAN, GARY
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD (
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
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CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARL W.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
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TYPE: DNA
ORGANISM: Zea mays
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100.0%; Pred. No. 0.013;
ative 0; Mismatches
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Pred. No. 0.011;
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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2:
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: DMA; ORGANISM: Zea mays
US-10-713-381-2
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; Sequence 3, Application US/10713381
; Publication . US20040221331A1
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               SEQ ID NO 90
LENGTH: 1304
TYPE: DNA
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Best Local Similarity
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Publication No. US20020183500A1
GENERAL INFORMATION:
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
                                                                               TITLE OF INVENTION: Compositions and Methods Relating FILE REFERENCE: DEX-0273 CURRENT APPLICATION NUMBER: US/10/001,857 CURRENT FILING DATE: 2001-11-20 PRIOR APPLICATION NUMBER: 60/252,054 PRIOR FILING DATE: 2000-11-20 NUMBER OF SEQ ID NOS: 208
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TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 158
TYPE: DNA
ORGANISM: Zea mays
                                                                 SOFTWARE: PatentIn version 3.1
ORGANISM: Homo sapien
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26; Conser
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: Sun, Yongming
: Liu, Chenghua
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Chen, Sei-Yu
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Pred. No. 0.013;
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Matches
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GENERAL INFORMATION:
                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17676, Application US/10741600 Publication No. US20050026169A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHBIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                             SOFTWARE: Fast
3Q ID NO 17676
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(1980)90)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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LOCATION: (1)...(19800
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1948918 ATTCTTGCTGAACAGTTCGTCTTGTACCA 1948890
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LE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
LE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
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                                      2 ATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                   FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                              Conservative
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                                                                                            70.0%;
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                                                                       Score 21; DB 8; Len
Pred. No. 2.2e+02;
                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21; DB 8;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                              Length 1980090;
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; ORGANISM: Arabidopsis thaliana US-09-938-842A-1624
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US-09-938-842A-1624
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US-09-938-842A-1624
                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1624
                                                                                      Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  equence 1624, Application US/09938842A ublication No. US20040009476A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/938,842A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: Harper, Jeff
PPLICANT: Kreps, Joel
PPLICANT: Wang, Xun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PELICANT: Zhu, Tong
TILE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TILE OF INVENTION: SAME; AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
LLE REPERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 1542
                                                                                                            Local Similarity
237 CATGATTGTTCAACCAATCGTCGGTTTCCA 266
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                                           CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                     68.0%;
80.0%;
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80.0%; Pred. No. 1
                                                                                                       Score 20.4; DB 3;
Pred. No. 1.5e+02;
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                                                                                      Mismatches
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                                                                                   Gaps
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US-10-282-122A-31883

Sequence 31883, Application US/10282122A Publication No. US20040029129A1

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APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Interest application of Essential Genes in Interest Application NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/20,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/2030,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
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                                                                                                                                                Sequence 1785, Application US/10260238 Publication No. US20040016025A1 GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
                                                                APPLICANT:
                                                                                                            APPLICANT: Budworth, Paul R. APPLICANT: Moughamer, Todd G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                 516
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Zamudio, c...
Zamodio, c...
Zamodio, c...
Zamodio, c...
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Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haselbeck,
Goff, Stephen A.
Katagiri, Fumiyaki
                                                                Briggs, Steven P.
Cooper, Bret
                                           Glazebrook, Jane
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                                                                                                                                                                                                                                                                                                                                                                                                                      67.3%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    0,
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; SEQ ID NO 1785
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-1785
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US-10-437-963-96639/c
                                                                                                                     RESULT 14
US-10-425-115-3534/c
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CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
                                                                                                                                                                                                                                                                                                                                                           US-10-437-963-96639
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NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 96639
LENGTH: 640
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Best Local Similarity
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                                                       Sequence 3534, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 6077
APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: PAT_MRT4530_94716C
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1179 TACATGTTTAACCGTTCGTCTTATTCAA 1206
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                                                                                                                                                                                                                                                                                                   Similarity
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Ricke, Darrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boukharov, Andrey A.
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82.1%;
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                                                                                                                                                                                                                                                                               Score 19.6; DB 7;
Pred. No. 2.9e+02;
0; Mismatches 4;
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Pred. No. 2.3e+02;
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                                                                                                                                                                                                                                                                                                                      Length 640;
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With

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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 3534

LENGTH: 901
TYPE: DNA
ORGANISM: Zea mays
FEATURE: IFORMATION: Clone ID: MRT4577_103225C.1
US-10-425-115-3534
                                                                      ₿
Search completed: March 6, 2006, 03:55:17 Job time : 45.1372 secs
                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-1977
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US-10-260-238-1977/c
                                                                                                                                      Query Match 65.3%;
Best Local Similarity 84.6%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 65.3%; Score 19.6; DB 8; Length 901; Best Local Similarity 84.6%; Pred. No. 3.1e+02; Matches 22; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                  ENGTH: 2000
                                                                                                                                                                                                                                                                                                                    OR APPLICATION NUMBER: US 60/370,620 OR FILING DATE: 2002-04-04
                                                                                                                                                                                                                                                                                                     R FILING DATE: 2002-04-04
BER OF SEQ ID NOS: 6077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ence 1977, Application US/10260238 ication No. US20040016025A1
                                                                                                                                                                                                                                                                                                                                                                                                                           OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION REFERENCE: 60111-NP TRANSPERS: US/10/260,238
TF FILING DATE: 2002-09-26
                                                                    291 CATGTTTAACCGTTCGTCTTATTCAA 266
                                                                                                                                                                                                                                                                                                                                                                        PPLICATION NUMBER: US 60/325,277
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                                                                                                       5 CTTGTTCAACCGTTCGTCTTGT
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                                                                                                                                                                                                                                                                                                                                                                                          CATION NUMBER: US 60/325,448 IG DATE: 2001-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Briggs, Steven P.
Cooper, Bret
Glazebrook, Jane
                                                                                                                                                                                                                                                                                                                                                       2001-09-26
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                                                                                                                                                         Score 19.6; DB 7; Length 2000; Pred. No. 3.4e+02;
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Result
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3: *
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US-10-523-503-37

US-10-330-773-86

US-09-925-065A-811550

US-09-925-065A-772237

US-09-925-065A-787145

US-09-925-065A-423

US-10-750-185-52713

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US-09-925-065A-70688

US-09-925-065A-70688
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US-09-925-065A-663899

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US-09-925-065A-472473

US-09-925-065A-936359

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US-09-925-065A-936397
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/US06_NEW_PUB.seq:*
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Sequence 863989,
Sequence 863989,
Sequence 5, Appli
Sequence 472473,
Sequence 936359,
Sequence 936359,
Sequence 936397,
Sequence 933397,
Sequence 85, Appl
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Sequence 98, Appl Sequence 211, App Sequence 7828, Ap	Sequence 1, Appli Sequence 13311, A Sequence 13295, A Sequence 212, App	Sequence 704153, Sequence 704154, Sequence 704155, Sequence 357, App Sequence 358, App	O	Sequence 819344, Sequence 821053, Sequence 30379, A Sequence 30379, A Sequence 9774, Ap Sequence 9787, Ap

## ALIGNMENTS

RESULT 1 US-11-136-527-2272

Sequence 2772. Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION: APPLICANT: Wyerh APPLICANT: Wyerh APPLICANT: Wyerh FILE REFERENCE: 031896-041000 (AM101086) FILE REFERENCE: 101806-05-25 FILE REFERENCE: 101806-05-25 CURRENT FILING DATE: 2005-05-26 FRIOR APPLICATION NUMBER: US 60/574,294 FRIOR APPLICATION NUMBER: US 60/574,294 FRIOR FILING DATE: 2005-05-26 FRIOR FILING DATE: 2005-05-26 FRIOR FILING DATE: 2005-05-26 FRIOR FILING DATE: 2006-05-26 FRIOR FILING DATE: 2006-05-26 FRIOR FILING DATE: 2006-05-26 FRIOR APPLICATION NUMBER: US/09/925,065A FRIOR APPLICATION NUMBER: US/09/925,065A FRIOR FILING DATE: 2000-10-24	*						
	plication US/09925065A, 0040181048A1 avid G; Identification and Mapping Collectide Polymorphisms 8827.135 NUMBER: US/09/925,065A B: 2001-08-08 NUMBER: US 60/243,096 2000-10-24	1 CARGCTTGTTCAACCGTTCGTCGTTGTTCC	atch 64.7%; Score 19.4; DB 12; Length 2422; cal Similarity 79.3%; Pred. No. 28; 23; Conservative 0; Mismatches 6; Indels 0; Gaps	SEQ ID NO 2272  LENGTH: 2422  TYPE: DNA  CORGANISM: Rattus norvegicus US-11-136-527-2272	LILING DATE: 2005-0: LICATION NUMBER: US LICATION SEQ ID NOS: 362830 SEQ ID NOS: 362830	William M Probe Arrays For Expression Profiling of Rat 896-041000 (AM101086) NUMBER: US/11/136,527	US-11-130-327-227 ; Sequence 2272, Application US/11136527 ; Publication No. US20050287570Al ; GENERAL THOOPENATON:

e 423, App e 52713, A

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APPLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human G.

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-05-09
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US-09-925-065A-546217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-925-065A-546217
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-863989
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 863989
                                        GENERAL INFORMATION:

APPLICANT: De Le Fuente Jose de Jesus
APPLICANT: Kocan Katherine M.

APPLICANT: Garcia-Almazan Consuelo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 546217
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                                                                                                                                         Sequence 5, Application US/11197133A Publication No. US20060040361A1
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Best Local Similarity
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Publication No. US20040181048A1
  TITLE OF INVENTION:
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                        Garcia-Almazan Consuelo Blouin Edwin F.
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Protective antigens and vaccines for the control of multi species
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Pred. No. 31;
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Gen
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
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Sequence 472473, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 10/972789
PRIOR FILING DATE: 2004-10-25
PRIOR APPLICATION NUMBER: US 10/425563
PRIOR FILING DATE: 2003-04-29
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NAME/KEY: misc feature

LOCATION: (1789)..(1789)

OTHER INFORMATION: n is a c g
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LOCATION: (1623)..(1623)
OTHER_INFORMATION: n is a c g
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LOCATION: (1606)..(1606)
OTHER INFORMATION: n is
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LOCATION: (1762)..(1762)
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LOCATION: (1595)..(1595)
OTHER INFORMATION: n is
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for Windows Version 4.0

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APPLICANT: Wang, David G.
ITILE OF INVENTION: Identification and Mapping of Single
ITILE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
(CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR PRIOR FILING DATE: 2000-11-20
PRIOR PRIOR DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PRIOR DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/251,766
                                                                                                                                                                                                                                                                                                                                                              RESULT 7
US-09-925-065A-936360
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SEQ ID NO 936359
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Best Local (
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PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION... Nucleotide Polymorphisms in the Human Genome
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SEQ ID NO 472473
LENGTH: 520
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al Similarity 76.7%;
23; Conservative
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76.7%;
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Pred. No. 3
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Pred. No. 37;
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    LENGTH: 1908
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US-10-523-503-37/c
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US-09-925-065A-936360
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Best Local S
Matches 23
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Matches 23
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Publication No.
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Publication No. US20040181048A1
                                                          APPLICANT: BASE PLANT SCIENCE GMBH
TITLE OF INVENTION: SUGAR AND LIFID METABOLISM REGULATORS IN PLANTS IV
FILE REFERENCE: 16313-0236
CURRENT APPLICATION NUMBER: US/10/523,503
CURRENT FILING DATE: 2005-02-02
                                    PRIOR APPLICATION NUMBER: US 60/400,803 PRIOR FILING DATE: 2002-08-02
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
NUMBER: FRANKE: FRANKSEQ for Windows Version 4.0
OFTWARE: PatentIn version 3.2
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TH: 593
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Pred. No. 38;
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US-09-925-065A-811550; Sequence 811550; Application US/09925065A; Publication No. US20040181048A1
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; ORGANISM: Arabidopsis thaliana
US-10-523-503-37
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Best Local Similarity 76.,
23; Conservative
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SEQ ID NO 86
LENGTH: 128963
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Publication No. US20060040262A1
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                                                                                SEQ ID NO 811550
LENGTH: 599
TYPE: DNA
ORGANISM: Homo sapiens
-09-925-065A-811550
                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08 PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR FILING DATE: 2000-10-24 PRIOR APPLICATION NUMBER: US 60/252,147 PRIOR FILING DATE: 2000-11-20
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APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILLING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum.
FILE REFERENCE: 108827.135
                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
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NUMBER OF SEQ ID NOS: 957086
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OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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                                                                                                                                                            APPLICATION NUMBER: US 60/289,846
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76.7%;
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; Pred. No. 51;
0; Mismatches
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Pred. No. 1.5e
0; Mismatches
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US-09-925-065A-787145/c
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; ORGANISM: Homo sapiens
US-09-925-065A-772237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08 PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR FILING DATE: 2000-10-24 PRIOR APPLICATION NUMBER: US 60/252,147 PRIOR APPLICATION NUMBER: US 60/250,092 PRIOR APPLICATION NUMBER: US 60/250,092 PRIOR APPLICATION NUMBER: US 60/261,766 PRIOR APPLICATION NUMBER: US 60/261,766
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 772237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 772237, Application US Publication No. US20040181048A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 787145, Application US/09925065A Publication No. US20040181048A1
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NUMBER OF SEQ II
SOFTWARE: FastSI
SEQ ID NO 787145
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                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                           PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
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Pred. No. 60;
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Pred. No. 59;
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; TYPE: DNA; Homo sapiens US-09-925-065A-787145

Query Match Best Local (

Similarity

61.3%;

Score 18.4; | Pred. No. 60; | O; Mismatches

DB 6; Length 629;

6; Indels 0; Gaps

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-423
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Best Local Similarity 78.6%;
Matches 22; Conservative
PRIOR APPLICATION NUMBER: US 60/437,482 PRIOR FILING DATE: 2002-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JRRENT APPLICATION NUMBER: US/09/925,065A
JRRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLE OF INVENTION: Identification and Mapping of Single TLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                    nce 52713, Application US/10750185 cation No. US20050260603A1
                                                                                                                                                                                                                                                                         CANT: MMI GENOMICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 recrirecrecarrecrerrrecea 322
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                                             APPLICATION NUMBER: US/10/750,185 FILING DATE: 2003-12-31
                                                                                             P: DeNISE, Sue K.

P: KERR, Richard

P: ROSENFELD, David

P: HOLM, Tom

P: HOLM, Tom

P: BATES, Stephen

P: PANTIN, Dennis

INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
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CATION NUMBER: US 60/261,766
IG DATE: 2001-01-16
IG DATE: US 60/289,846
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Pred. No. 60
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; TYPE: DNA ; ORGANISM: Bovine 19866881292329 US-10-750-185-52713

Query Match Best Local Similarity

61.3%; Score 18.4; 78.6%; Pred. No. 67

DB 8;

Length 1012;

0; Gaps

0;

Matches 22; Conservative 0; Mismatches 6;
2 ANGCTIGHTCAACCGTTCGTCTTCTTCC 29

Db 454 ATTCTTGTTTAACCGTATTTCTTGCTCC 481
Search completed: March 6, 2006, 10:32:51
Job time: 31.3166 secs

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Result
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 1.0
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AC15206 Oryza satura
AC184290 Homo sapi
AL807784 Mouse DNA
AC157528 Pan trogl
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AC164520 Pan trogl
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                                       RESULT 2
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Sequence 5 from Patent WO0160997.

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PAT 10-SEP-2001

AX224398.1 GI:15554640

Zea mays

1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40

AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC

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d Kendall,T.L.	Huffman,G: and and method of w	naat,C.W., oxy region -2001; INC. (US)	.W., Garr regulatos 23-AUG-VATIONAL, lifiers la mays" sa mays con:457,7"	Fox, Terred Property of the Total Property o	n,M.C., Fox,T.W sue-preferred r. WO 016997-A 6: WO 016997-A 6: Location/Quali: Location/Quali: 1.40 /organism="Zea /mol_type="una: /db_xref="taxo;	rtsen tiss tt: WG BER H	· · · · · · · · · · · · · · · · · · ·	AUTHORS TITLE JOURNAL FEATURES SOURCE SOURCE	OR E
Tracheophyta; aceae; PACCAD	mbryophyta; Poales; Po	Streptophyta; E yta; Liliopsida; pogoneae; Zea.	idiplantae, Strepto Magnoliophyta, Lil deae, Andropogoneae				Zea may Zea may Eukaryo Spermat Clade;	SOURCE ORGANISM EFERENCE	RE SC
PAT 10-SEP-2001	linear F	bр DNA 997.	40 b nt WO01609	Patent 15554641	from	AX224399 Sequence 6 AX224399 AX224399.1	AX2 Seq AX2 AX2	RESULT 1 AX224399 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS	222222
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.34013 Rattus no .30117 Rattus no	AC134 AC130	73	AC134013 AC130117	14	196990	56.5	22.6	4. 4. 5.	o.
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                                                                                                                                                                                                                                                                                                                                                                          Male tissue-preferred regulatory region patent: WO 0100997-A 3 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US) Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              Albertsen, M.C.,
                                                                          Zea mays
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 tissue-preferred
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                                      Panicoideae;
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/mol_type="unassigned
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/mol_type="unassigned
/db_xref="taxon:4577"
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Patent W00160997.
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Patent WO0160997,
              Fox, T.W.,
                                     Andropogoneae;
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.W., Garnaat,C.W., regulatory region
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Pred. No. 0.0001;
Mismatches 0
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                        BD062177
BD062177.1 GI:22607782
JP 2001520523-A/2.
                                                            BD062177 1394 bp Male tissue-preferred regulatory
   Homo
              Homo sapiens (human)
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Best Local Similarity
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                                                                                            1239 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
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PP 19-UN-1998 JP 1:
PR 23-UN-1997 US
PR 23-UN-1997 US
PI TIMMY L KENDALL
PC C12N15/82,C12N15
,C07K14/34,C12Q1/68,
PC A01H5/0
CC Strandedness: Sin CC Topology: Linear FH Key
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PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
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1 (bases 1 to 1394)
Albertsen,M.C., Fox,T.W., Garnaat,C.W.,
Kendall,T.L.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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23-JUN-1997 US 08/880499
MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAT,GARY A HUFFWAN,
TIMMY L KENDALL
C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC
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sapiens

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REFERENCE AUTHORS

Hominidae; Homo Eukaryota;

COMMENT

JP 2001520523-A/2

PN JE PD 30 PF 19 PR 23 PF MF PI MF PI 71 PC C1 PC C1 PC St CC TC

Strandedness: Single; Topology: Linear;

Location/Qualifiers.

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/mol\_type="genomic DNA"
/db\_xref="taxon:9606"

/34,C12Q1/68,

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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Location/Qualifiers
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Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and
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23-JUN-1997 US 08/880499
MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Butheria; Euarchontoglires; Primates; Catarrhini;
           PAT 10-SEP-2001
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Zea mays
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1 (bases 1 to 3343)

Pox,T.W., Trimmell,M.R. and Albertsen,M.C.

Cloning of Ms45, a gene required for male ferility from Zea mays
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Hi-Bred Intl. Inc., 7300 N.W.
IA 50131-1004, USA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2 from Patent W00160997.
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AX224395.1 GI:15554637
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ilarity 100.0%; Pred. No. 6.2e-05
Conservative 0; Mismatches
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|oin(1392. .1768,1898. .2182,2280.
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RESULT 8 AX224395 LOCUS

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1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC

AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC

1278 40 Indels ORIGIN

Matches Query Match

40;

Local

Similarity

100.0%; llarity 100.0%; Conservative 0

0;

Score 40; DB Pred. No. 6.2 0; Mismatches

DB 6; Le.. . 6.2e-05;

Length 1394;

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REFERENCE AUTHORS TITLE

SOURCE ORGANISM KEYWORDS

ERSION

AX224394.1

FEATURES

source

/organism="Zea mays" /mol\_type="unassigned DNA" /db\_xref="taxon:4577"

JOURNAL

RESULT 7
AX224394
LOCUS
DEFINITION
ACCESSION

AX224394
Sequence 1 from Patent
AX224394

1394 bp : WO0160997.

DNA

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ORIGIN

source

Matches Query Match

40;

Similarity

100.0%; Score 40; DB 6; I llarity 100.0%; Pred. No. 6.2e-05; Conservative 0; Mismatches 0;

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RESULT 10  NECOMMENT  PROBLEMS  REPUBLIS  REPU	TGELYVADAYYGLMVVGQSGVASSVAREADGDPIRFANDLDVHRNGSVFFTDTSMRY SRKDHLNILLEGEGTGRLLXYDEFTSGVHVVLKGLVFNGYGISEDHQFLLFSETTYC RIMRYMLEGFAGEVEVFANLPGFFDNVRSNGRGQFWANIDCCRTFAQEVFAKRPWLR TLYFKFPLSLKVLTWKAARRWHTVLALLDGEGRVVEVLEDRGHEVMKLVSEVREVGRK ORIGIN  QUERY Match Best Local Similarity 100.0%; Score 40; DB 15; Length 3343; Best Local Similarity 100.0%; Pred. No. 5.4e-05; Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 40; Conservative 10; Mismatches 0;  AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
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JOURNAL COMMENT FEATURES SOURCE	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL TITLE JOURNAL	RESULT 11 AC135206/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	Query Match Best Local Matches: 3  Qy 1  Db 36341
	ubnission  yu.Y. Soderlund,C., K. and Thompson,S. K. and Thompson,S.  ubnission  d (11.JAN-2003) Arizona 303 Forbes, Tucson, AZ 303 Forbes, Tucson, AZ yu.Y., Soderlund,C., , Henry,D., Thompson,S.,  ubnission	Yu, Colling (09-00) Tu, Colling (09-00) Tu, Colling (09-00) Tu, Colling (09-00) Tu, Colling (09-00)	AC135206 137327 bp DNA linear PLN 16-APR-2003 Oryza sativa (japonica cultivar-group) chromosome 3 clone OJ1041P02, complete sequence. AC135206 AC135206 AC135206.3 GI:27596977 HTG. Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group) Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaa. 1 (bases 1 to 137327) Wing,R.A.; Yu,Y., Soderlund,C., Kim,HR., Rambo,T., Currie,J. and Collura,R.A.; Yu,Y., Soderlund,C., Kim,HR., Rambo,T., Currie,J. and Collura,R.	Query Match 76.0%; Score 30.4; DB 15; Length 110000; Best Local Similarity 85.0%; Pred. No. 0.18; Matches: 34; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  1 AGGATACCTACTCCCAAACAATCCATCTATCCATCCATCC

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VSI I AKYAVPAGEWPELL PF I FQCSQSP DEDDIREVALIL JES SI TI DHSHLVRRASANV
VSI I AKYAVPAGEWPELL PF I FQCSQSP DEDDIREVALIL JES SI TETI GTTFQSHLNDL
QPI LLKCLQDEASSRVBI AALKAVGSF I EYVNDGGDVVKI FRD PVPS I LANVSRQCLAN
GEEDVAS I AFEI FDELL ES PAPLIGDS VRSI VQPSLEVCNQELEINI RQQAI QI I SW
LVKFKAS FLKKHKLVI PI LQVMCPLITETADEDGDSDLAADRS AAAEVI DTMA I NLPRH
VFP PVLEFASVSFRI INFX Y REAAVTSLGOVSEGCCEHLKOKLEDCLKVVLEALKOGE
QMVRQAAS FALGQFAEHLQPEI LSHYESVLPCI LNALEDPS DEVEKSYYALAAFCED
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DVNDEPRVRNI SWLTI I ADI LTAI RAI FP PAHADVLEKQKD I LDTVMNI Y KTMREDDD
KEVNAQACTSLAD I VROCGFA I I SEP I TKLEDSTLEKQKD I LDTVMNI Y KTMREDDD
KEVNAQACTSLAD I VROCGFA I I SEP I TKLEDSTLEKQKD I LDTVMNI Y KTMREDDD
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DKDVLMDAVSDLL PAFAKVMGSYFD P I TKLEDSTLEKGKD I LOTVMNI Y KTMREDDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .16878
emu(join(26563. .26772,27082. .27288,27430. .2753
.27940,28051. .28126,28327. .28484,28616. .28678,
.28874,29560. .30575))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .9495)
                                                                                                                                                                                .30575)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaijin/Gaigin-like"
                                                                               .27537,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .13826,
                 맑
                                                                        S
                                                                                                                                                 Query Match
Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                    119478 AGAACACCTACTCCCAAACAATCACGCTGACTCATGCAAC 119439
                                                                                                                                                    34;
                                                                                  Ь
                                                                                                                                                                                       Similarity
                                                                               AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                /note="putative MITE, Castaway-like"
complement (59793. .62196)
/gene="OJ1041F02.6"
                                                                                                                                                                                                                                                                                                                                                                                            51474. .51836
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ASSICTERASLESSEGHERVURGNI TYNGSMYGREGOTALLWTDKYRFETAAQVCARKHYKE
LNEWLKGWDERGHRUKGNI TYNGSMYGREGOCOCHTYSEDASDYENVLLI TGEFVGC
KSAAVFACAREGGENVI ELIMPEKTVVFPET FLENKLLAGTLDLKEDKLHDSSHESI KYI
PTRVFYHMIRKSI I SI SAHSSSLSVI KLHCL VNTSDMRRGA YVRQKFEBATKSHGLEK
WSQEBI I GLD I SINSLDPASGTPGTARYKQVINKTLI LFEDDDTYVFDEDBGFI STILKM
VETTKWPI I LTSNKKDPPLEHLLAQL VLD DTYPESBELLSHVDMI CKSEGVEI TVPAG
KHI IDAFLGRLINKCLSCPSLLDLDAVHSTVPRIMPWDFPCKLSET I YMBLDKTI VYAE
QKKKQMEVSEFEGLELOIMTPLTKGRASGKTRKPKKSKLHGBRADCNDASPCKNDLD
DFHDSPDI FLFSNHQRMRNRRGVVLFARSBDDLLADAHAAKDATFTVQGGRLLFOSSEL
PCLYGHGISNI VDESV FFQQSSYPHLHREVI SNQLCFPSSSRA FEPASS FQNQLESNM
PGSI SQLCDTFMSQGISCVPERSSFMVGGTSASI SSDDLLSSLVSNGLSALRNESTYTA
SVVALEDTINKVENQMTDKPGKCMEDEVGETCBAYVELADRUNDHASCS I TGYQLMDECS
RAESVHILSGKKNDSCKVEHYQDTWRKLRQCHPVLPCOMNHRIBSVSGALKRVSRVSD
LI SESDLMLI SCHPESSDI SDPSLTFYTESDGFSYSKOLEMGSI YAGHGIC I FLODSQ
ATDDGFVDFLQELLFSGTTTTSLGKFVSSGI SCGDGSGNI SHVKYPTSCI SKRRERQA
RLREVLLDVVPPKLSQSLIGHPAFVDYLSSMSQI SQLENNGLSECKASSKQRRCRQPRH
YLSSGALSLSAEDIGLLAQCSTFSDRRESETI I EQAIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="hypothetical protein"
complement (join (3504) . 35184, 35866 . .36033, 36922 . .3720;
complement (join (3504) . .35184, 35866 . .40287, 40406 . .40617,
37280 . .38523, 40038 . .40104, 40196 . .40287, 40406 . .40517,
41678 . .41760, 42229 . .42259, 42907 . .43088, 43694 . .43753,
44229 . .44426, 44622 . .44676, 45877 . .45992, 46149 . .46313,
46447 . .46620, 47271 . .47470, 47915 . .48019, 48200 . .48263,
49589 . .49855) )
/gene="OJ1041F02.5"
/note="putative MITE, MITE-adh,
39681. .39879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Godon_start=1
/product="hypothetical protein"
/protein id="Appl6848.1"
/protein id="Appl6848.1"
/db_xref="01:29893594"
/translation="MGGSADPEAPTPTPSPSPSPAKATPSPASADGNRLRRCVQSKLS
WGPPFKAGGGGEAGGAGLPPLAAGDGTPEKVKKRGRPRKSEAGKKPSSNRETTGLEQD
SKDEVILVDESPQKKQRKGRGKNQGAALKVPNRKHCKALESTDERSEAGIAERSQTQA
VLPQKS9TSVNIDLYGPSEASPVNDNVDALDNEDKPGLIVDLRSEAGIAERSRFLS
SGKKWHIPFASARKIHKGAGQDILNVEDEDMISICAFERDPPLCPVHVLYELEVTMPIH
WSNKWLIADKSFLGTSTTEQNSAEHADPGKHLANFHDKQNKSKFSQDVIDUDECLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="putative MITE, MITE-adh, type D-like" complement (3168 . .31815) complement (35049 . .49855) /gene="OJ1041F02.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGISDEGVFFAVKEVCLCDQGSNAQQCIFQLEQEIALLSQFEHENIVQYYGTDKEDSK
LYIFLELVTQGSLASLYQKVELRDTHYGSYTRQILNGLTYLHENIVHRDIKCANILV
HANGSVKLADFOGLAKEITKFNVLKSCKGTVYMAPEVVNFKTERNIVHSLGCTVL
EMLTRQLFYFGLEWTQALTKRIGKGEPAIFNCLKSDARDFISQCVKFNADDRESAAKU-
LEHPFVNRSNRSIRSMRTSSRSNSSILVLLIMWSWPGRTIRYREAILSTAQSSTFTIA
FHLLILSHSLLRGDMSWFSQRLIFSPENRLNVHSSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVADWEAHKAGRSSFSSSASTPKPREEPPARDSPVRREVAAEEEEPPSLPAPAAAPVLP
AKETPRIVALEAPAFLLRVDDWEPAREDVRKASGEGGIKGVREPEVVLKREPESMVRPA
VCYVESTMOILRSFAPEEDSHAHAFAARSGGGDACQDAGEEEDDDAAAVLILEELRIGE
TSEEFTGTSSLSTTNDDETSSTTTESMFYISPNGRFRRKIRSMNRGMLLGSGSFGTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="mgppaappspsssssggssrrrrlerrnaakhigydasnfcayp
Qsppaasapasgspslacspacsldltsfriggsgdgcrdvqllcsslglsgvddfav
                                                                                             39012. .39207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27679.
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/db_xref="GI:29893593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="0J1041F02.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
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                                              type M-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .36033,36922. .37205,
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/note="putative MITE, MITE-adh, type G-like"

76.0%; 85.0%;

Score 30.4; DB 15; Pred. No. 0.17; Mismatches

0

6

Indels

<u>.</u>

Gaps

0

Length 137327;

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TITLE
JOURNAL
REFERENCE
AUTHORS
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VERSION
KEYWORDS
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AC156670
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOWIS, C., KTAIT, C.L., LEDOW, H., LEVALL, J., LANDOW, H., LEVALL, J., L., LANDOW, H., LEVALL, J., L., LANDOW, H., LORGER, S., LOPEZ, J., LIU, X., MA, J., LORGEN, P., LORGER, S., LU, X., MA, J., MARDESHWARI, M., MAININGARINE, M., MARINGOLD, K., MARINGOLD, K., MARINGOLD, K., MARINGOLD, K., MARINGOLD, K., MARTIN, K., MARTIN, R., MARTINEZ, E., MARINGOLD, K., MARTIN, R., MARTINEZ, E., MARINGOLD, K., MORIS, S., MARINGEY, S., MCLEOD, M., MCLEOD, M., MOREILL, T.Z., Meenen, E., MILOSAVIJEVIC, A., MINGER, G., MINJA, E., MONTEMBYOT, J., MOORE, S., MINJA, E., MORTIS, S., MOTGIS, S., MOTGIS, S., MOTGIS, S., MORTIS, S., MORGEN, M., MORTIS, S., MORGEN, M., MORTIS, S., MOTGIS, S., MORGEN, M., MORTIS, S., MORGEN, M., NORTIS, S., MORGEN, M., NORTIS, S., MORGEN, M., NORTIS, S., MORGEN, M., NORTIS, S., MARINGHON, M., PEREZ, A., PEREZ, L., PÉRMINGOL, C., PIRME, S., P., L., L., PLUZO, M., QUICOZ, J., RCHININ, G., PEREZ, L., PÉRMINGOL, C., PIRME, S., M., GARLEY, M., REGIM, R., ROSE, R., RULZ, S. J., SARLEY, M., REGIM, R., ROSE, R., RULZ, S. J., SARLEY, J., SHELTY, J., SCHETEZ, S., SCOLT, G., SHASTMAN, S., SHEN, H., SHELTY, J., SHELTY, J., SHELTY, J., SHEN, M., STEODS, R., SORG, K., Z., SCRELLER, C.D., SMAJS, D., SHELTY, J., SHECH, M., STEODS, R., SHELTY, J., SHECH, R., SORG, K., Z., SCRELLER, SORS, J., USMANI, K., VALAS, R., VEZA, V., VILLBABA, D., WALGON, L., WALKE, B., WANG, J., WALGON, L., WALKE, B., WANG, J., WALSON, L., WALKE, B., WALLEY, R., WOOGEN, H., WOOLLY, K., WALLEY, R., WOOGEN, H., WOOLLY, K., WALLEY, R., WOOGEN, H., SMILL, H.O., WALKER, R., WOOGEN, H., K., WOOLLY, K., WALLEY, R., WOOGEN, H., K., WOOLLY, K., WALLEY, R., WOOGEN, H., K., SMILL, H.O., WALKER, R., WOOGEN, H., K., WALLEY, R., WOOGEN, H., K., SMILL, H.O., WALKER, R., WOOGEN, H., K., SMILL, H.O., WALKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M. Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B., Cardensay, C., Catter, K., Cavazos, I., Cessar, H., Center, A., Chen, S., Chen, S., Chen, S., Chen, S., Chen, S., Chen, S., Chen, C., Chen, S., Duplan, A., Durbin, K., Duval, B., Eaves, K., David, M., L., Davis, C., Dedetich, D., Delgado, O., Denson, S., Denn, A., Durbin, K., Duval, B., Eaves, K., Delgan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Ernnedez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Guerra, W., Guerra, W., Guerra, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gebrergergis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guerra, S., Haladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jacob, L., Jacob, L., Jacob, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kally, S., Khan, Z., King, L., Kovar, C., Kowls, C., Kraft, C.L., Lebow, H., Levan, J., Lews, L., Li, Z., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Lorensublewa, L., Loulseced, H. Tozano, R., Ton, Y., Ton, S., Liu, J., Lorensublewa, L., Loulseced, H. Tozano, R., Ton, Y., Ton, S., Liu, J., Lorensublewa, L., Loulseced, H. Tozano, R., Ton, Y., Ton, S., Liu, J., Liu, 
      2 (bases 1 to 303308)
worley, K.C.
Direct Submission
Submitted (03-FEB-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V
Yu,R., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muzny,D.Marie, Metzker,M.Lee., Abramzon,S., Add
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Angul
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC156670
AC156670.2 GI:68266432
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (cow)
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Bos taurus clone CH240-60K24, *** SEQUENCING IN PROGRESS ***, 48
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unordered pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 303308)
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On Unn 28, 2005 this sequence version replaced gi:58531390.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by slzed gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Direct Submission
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This sequence may represent more than one clone.
Consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will
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Center project name: FDDI
Center Clone name: CH240-60K24
------- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 284059 bases at least Q40
Consensus quality: 284379 bases at least Q30
Consensus quality: 284397 bases at least Q20
Consensus quality: 2843897 bases at least Q30
Consensus quality: 2843897 bases at least Q30
Consensus quality: 284313 bases at least Q30
Consensus quality: 284413 bases at least Q30
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Center code: BCM
Web site: http://www.hgsc.b
Contact: hgsc-help@bcm.tmc.c
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138: contig of 6918 bp in length
121: contig of 5333 bp in length
40: contig of 9669 bp in length
90: gap of 50 bp
16: contig of 15770 bp in length
13: gap of 473 bp
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16: contig of 9213 bp in length
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16: gap of 1500 bp
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10: gap of 158 bp
10: contig of 158 bp
11: contig of 1590 bp in length
12: contig of 1590 bp in length
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BAC Library)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alsbrooks, S.L., Amaratunge, H.C., Are, J.K., Myle, M., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Barkenburg, K., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Buouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burett, C., Burch, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burcht, K.L., Bydd, N.C., Chen, G., Chen, E., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Delgado, C., Davy-Carroll, L., Dederich, D.A., Dellaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Dellaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Dellaney, K., Gabisi, A., Gare, R., C., Elhaj, C., Emerling, S., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Earnhart, C., Edgar, D., Bawards, C.C., Elhaj, C., Berzi, N., Gill, R., Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Hollows, C., Lich, J., Hernandez, J., Homai, F., Howard, S., Huber, J., Harris, R., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hernandez, O., Kodson, E., Karlsson, E., Kalsson, E., Karlsson, E., Massey, E., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Luar, R., Martindale, A., Martinez, E., Massey, E., Mahhiney, E., McLeed, M., P., Meador, M., Mei, G., Merscher, S., Mawhiney, E., McLeed, M., P., Martindale, A., Martinez, E., Massey, E., Mashiney, A., Western, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Stason, I., Soderer, S., Scott, G., Shan, H., Shim, C., Shoshitari, N., Stason, I., Stason, R., Martin, A., Stane, M., Thomas, S., Marte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.

1 (bases 1 to 55001)

1 (bases 1 to 55001)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,

Alsbrooks,S.L., Banton,J., Binage,K., Blankenburg,K., Bonnin,D.,

Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
                          Direct Submission
Submitted (28-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Mar 28, 2002 this sequence version replaced gi:19747063.
                                                                                                                                                                                Submitted (27-MAR-2002) of Molecular and Human G Baylor Plaza, Houston, T 4 (bases 1 to 55001)
                                                                                                                                                                                                                                                                                                                                                              Submitted (21-OCT-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 55001)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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AC084290.15
                                                                                                                                                                                                                                                                                       Worley, K.C.
Direct Submission
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                                                                                                                                                           Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          INFORMATION: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                    lor Plaza, Houston, (bases 1 to 55001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:19774277
                                                                                                                                                                                                           ) Human Genome Sequencing Center, Department
Genetics, Baylor College of Medicine, One
TX 77030, USA
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are onl sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and

local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity expect < le-34) to the (Nuc. Acids Res. 25:3389-3402) similarity (expect < le-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguitles or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguitles. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

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FEATURES
             repeat_region
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                                                                                                  /rpt_family="MIR" 4938. .5053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                              rpt_family="AT_rich"
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                                                                                                                                                        family="L1MD3"
ement(400)
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Qy 4 ATACCT	Matches 27; Conser	y Matc	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region		l l	repeat region	repeat_region	repeat_region			repeat region	repeat_region	repeat_region	repeat_region	repeat_region		repeat region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	
ATACCTACTCCCAAACAATCCATCTTACTCAT 35	vat	60.0%;	complement (2314723327)	27962309	268222789	32 fami	235922632 rpt family="	.22358	221792680 221792680 /rot family="(TAAAA)n"	complement (2066020753)	1913619158 /rpt family="AT rich"	l 🗁	ch"	amily="Alusx"	<pre>/rpt_tamily="AluJb" complement(1830918606)</pre>	complement (1762417922)	1618616413	<pre>/rpt_family="MIR"</pre>	family="MIR"	/rpt_tam11y="MER45" 1441114545	814219	13737	lement (12	1279712828 /rpt family="(CATATA)n"	/rpt_family="MIR"	/rpt_family="MLT11" 1194112179	11635	8.1	+n •	<sub>ff</sub> .7	<pre>complement(9151 . 9317) /rpt_family="LTR43"</pre>	

밁 47598 AAACTTACTCCCAAACAATCTATGTCACTCAT 47567

> 0; Gaps

0;

KEYWORDS SOURCE ORGANISM ACCESSION VERSION RESULT 14 AL807784/c LOCUS DEFINITION sequence. AL807784 AL807784 127196 r Mouse DNA sequence from clone HTG.
Mus musculus (house mouse)
Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; AL807784.11 GI:25045332 127196 bp DNA linear ROD 13-NOV-2002 om clone RP23-448C18 on chromosome X, complete

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REFERENCE
AUTHORS
TITLE
                                                                                                            VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                    RESULT 15
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                                                                                                                                                        ACCESSION
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                                                                  ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: RMBL; Sw., SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep RP23-448C18 is from the RPCI-23 Mouse PAC Library constructed by the group of Pleter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                 Pan troglodytes BAC clone CH251-422M6 complete sequence. AC157528
                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence dat from the whole genome shotgun alone has only been used where it has phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-NOV-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk Cnone version replaced gi:24939941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciurognathi; Muroidea; Muridae; Murinae; Mus
                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                Pan troglodytes
                                                                                     Pan troglodytes (chimpanzee)
                                                                                                                                   AC157528.2 GI:62000959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VECTOR: pBACe3.6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                            AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP23-448C18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
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                  Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                   chromosome unknown,
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AUTHORS
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AUTHORS
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JOURNAL
Query Match
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Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Forest Park Parkway, St. 3 (bases 1 to 154857)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson, R.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.bacpac.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAPPING INFORMATION:
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1 to 154857)
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                                                                                                                                                                                               clone_lib="CHORI251"
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                                                                                                                                                                                                                                                                                         _type="genomic DNA"
60.0%;
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Score 24;
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Direct Submission
Submitted (27-APR-2005) Washington University School of Medicine,
Semame Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO
                                                                                                                                                                                                            On Mar 30, 2005 this sequence version replaced gi:59933404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shah, N., Cotton, M. and Lewis, S.
The sequence of Pan troglodytes BAC clone CH251-422M6
Unpublished (2001)
                                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu
Center project name: C_AB0422M06
                                                         Contact: submissions@watson.wustl.edu
                                   Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics, Genome Sequencing Center, Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics, Genome Sequencing Center, 4444
. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, se see

The CHORI-251 Chimpanzee BAC library has been constructed at the Children's Hospital Oakland Research Institute, BACPAC Resources, by Dr. Baoli Zhu. DNA was isolated from white blood cells obtained from a male chimpanzee (Pan troglodytes, 'Clint', Yerkes #C0471; birthdate:-6-80). The clone and detailed information can be obtained from Pieter de Jong and co-workers at

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This sequence is the entire insert of the clone Location/Qualifiers
                                                                                                /note="Unresolved bases"
127657. .127881
                                                                     note="Sequence derived from one plasmid subclone."
                                                                                                                                                                                                                                                                                                                                organism="Pan troglodytes"
                                                                                                                                                                 note="Unresolved bases"
  B
  8,
Length 154857;
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Best Local Similarity 84.4%; Pred. No. 53;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 ATACCTACTCCCAAACAATCCATCTTACTCAT 35

Db 123632 AAACTTACTCCCAAACAATCTATGTCACTCAT 123663

Search completed: March 5, 2006, 21:55:48

Job time: 176.689 secs

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Result
No.
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Perfect score:
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AAH76333
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AAH76336
AAH76334
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Aah76332 Z. mays M
Aah76333 Z. mays M
Ac138730 Rice Stre
Ac138730 Rice Stre
Ac138730 Rice Stre
Ab132304 Human gen
Ab132304 Human imm
Adb54282 Pretreate
Ade84496 Human imm
Ada89580 Oligonucl
Ab213750 Arabidops
Ab132155 Human imm
Ab154304 Chemicall
Ab154304 Chemicall
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# ALIGNMENTS

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RESULT 2
ANAH76336
ID ANAH7
XX ANAH7
AC ANAH7
XX ANAH7
XX Z- T
DE Z- T
XX M845
KW Mybsi
XX Zea
XX Zea
XX Zea
XX W Mybsi
XX BPN W02(
PN W15-)
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Z. mays
                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -72 to -11 bases upstream of the TATA box of a Z. mays MS45 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

    mays Ms45 male tissue-preferred regulatory region fragment.

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d seed; ds.
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); Mismatches
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Pred. No. 4.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ms45; male tissue; regulatory region; transcription; male fertility;
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                                                                   Ms45; male tissue; regulatory region; transcription; hybrid seed; promoter; ds.
                                                                                                                                                      AAH76340;
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                                                                                                                                                                             AAH76340 standard;
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                                                                                                                                                                                                                                      AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 125
                                                                                                                                                                                                                                                                                                                                158 BP; 41 A; 50 C; 21 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WC,
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                  promoter;
                                                                                                                              (first entry)
                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WT,
                                                                                                                                                                             255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garnaat
                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                              Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ć.
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                 46 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huffman
                                                                                                                                                                                                                                                                                                 5e-06;
                                                                                                                                                                                                                                                                                                            DB 5; Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprising nucleotide sequences the MS45 gene useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ရ
                                                                                                                                                                                                                                                                                      <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kendall
                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                      Indels
                                                                                  male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H
                                                                                 fertility;
                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ξ
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23-AUG-2001. WO200160997-A2

13-FEB-2001; 2001WO-US004527

(PION-) PIONEER HI-BRED INT INC

Fox TW,

Garnaat CW,

Huffman G,

Kendall TL;

2

comprising nucleotide sequences the MS45 gene useful for

4

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Query Match
Best Local S
Matches 40
                                                                                                                                                                              19-JUN-1998;
                               New nucleic acid encoding a - useful in mediating plant
                                                                        WPI; 1999-105628/09
                                                                                                                                                      23-JUN-1997;
                                                                                                                                                                                                           30-DEC-1998.
                                                                                                                                                                                                                                                                                      Ms45; male; tissue-preferred; plant tissue; differentiated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a Z. mays Ms45 promoter fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
       Claim 2; Page 22-23; 39pp; English
                                                                                                                            (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                     WO9859061-A1
                                                                                                                                                                                                                                                               Zea mays
                                                                                                                                                                                                                                                                                                                            Zea mays Ms45 male tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                          08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                              AAX07408 standard;
                                                                                                                                                                                                                                                                                                                                                                                     AAX07408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 255 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Fig 8; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                  Fox
                                                                                                                                                      97US-00880499.
                                                                                                                                                                                98WO-US012895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 A; 86 C; 39 G; 71 T;
                                                                                                  ,WT
                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                            1394
                                                                                                  Garnaat CW,
                            M845 male tissue-preferred regulatory region fertility, especially hybrid seed production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                    regulatory region; plant cells;
maize; hybrid seed; fertility; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                 Huffman GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.3e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                 Kendall TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                              Query Match
Best Local S
Matches 40
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The sequence is that encoding region. It may be used in the

an Ms45 male tissue-preferred regulatory construction of a vector for a method of

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1239

AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1 Similarity 40; Conser

100.0%;

0;

Score 40; DB Pred. No. 6.8 0; Mismatches

6.8e-0 DB 2;

40 Indels Length 1394;

0,

Gaps

0

Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;

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RESULT 6
AAX07409
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                                                                                                                                                                                                Query Match
Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants
AAX07409;
                                AAX07409 standard; DNA; 1394
                                                                                                                                                                                                                                                                  Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                      1239 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
                                                                                                                                                           H
                                                                                                                                                                                              l Similarity
40; Conserv
                                                                                                                                             AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                              <u>,</u>
                                ВP
                                                                                                                                                                                                              Score 40;
Pred. No.
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                          6.8e-06;
thes 0;
                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                               Length 1394;
                                                                                                                                                                                              Indels
                                                                                                                                                                                            0,
                                                                                                                                                                                            Gaps
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WPI; 2001-514772/56

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The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dioot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile
                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding a - useful in mediating plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ms45; male; tissue-preferred; plant tissue; differentiated;
                                                                                                                                                                                                                                                                                    Claim 3; Page 23-24; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Albertsen MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9859061-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays Ms45 male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PION-) PIONEER HI-BRED INT INC
encodes a product select seeds are produced by plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fox TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-00880499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US012895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garnaat CW,
                                                                                                                                                                                                                                                                                                                                      Ms45 male tissue-preferred regulatory region fertility, especially hybrid seed production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulatory region; plant cells; hybrid seed; fertility; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huffman GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kendall
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AAH76317
AAH76317
AAH76317
AAH76317
AAA AAH7
AC AAH7
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene hapacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 martissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A male tissue-preferred regulatory region comprising nucleotide essential for initiating transcription of the MS45 gene useful f mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200160997-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M845; male tissue; regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z. mays Ms45 male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH76332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 46; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-FEB-2000; 2000US-00504487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-2001; 2001WO-US004527
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WO200160997-A2
                                                                                                                hybrid seed;
                                                                                                                                       M845; male tissue;
                                                                                                                                                                                              Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
                                                                                                                                                                                                                                                     29-OCT-2001
                                                                                                                                                                                                                                                                                                         AAH76333;
                                                                                                                                                                                                                                                                                                                                                               AAH76333 standard; DNA; 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fox TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue-preferred regulatory region encoding DNA.
                                                                                                                                                                                                                                                     entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 5; 1
Pred. No. 6.8e-06;
                                                                                                                                       region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huffman G,
                                                                                                                                          transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kendall TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                             male
                                                                                                                                             fertility;
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RESULT 9
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AC ACL3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an MS45 martissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                            22-JUN-2001;
24-AUG-2001;
26-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514772/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice stress-regulated promoter SEQ ID NO:17293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-2005
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                                                                                                      Kreps J,
                                                                                                                                                                                                         21-NOV-2001;
                                                                                                                                                                                                                                                                                                                                  21-JUN-2002; 2002WO-US019668
                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003008540-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              abiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                          SYNGENTA PARTICIPATIONS
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                                                                           Briggs SP,
T, Provart
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                                                                                                                                                                                                       ; 2001US-0300112P.
; 2001US-0314662P.
; 2001US-0325277P.
; 2001US-0332132P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stress tolerance; transgenic plant; plant; cereal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry
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                                                                           Cooper B,
N, Ricke
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Pred. No.
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                                                                                 Glazebrook J,
D, Zhu T;
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                                                                                                           Goff
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                                                                                                      Katagiri
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WPI; 2003-248011/24

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RESULT 10
ACN45146
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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (1) for screening drug candidates; (ii) for screening of bioactive agent capable of bioactive agent capable of modulating the activity of CAP; (iv) for sevening of evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (ivi) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
                                                                                                                                                                                                                                                                                    Recombinant nucleic acid useful for diagnosis comprises a nucleotide sequence.
                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1948; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-328604/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002; 2002US-00087192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genomic sequence hCG1639824.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SAGR-) SAGRES DISCOVERY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
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85.0%;
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Pred. No. 0
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0.047;
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                                                                                                                                                                                                                                                                                                           treatment
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        RESULT 11
ABZ10202/c
ID ABZ10
XX
AC ABZ10
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DT 16-JA
XX
The present invention describes a method for detecting and CC differentiating between hematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a cold in distinguishes between methylated and non-methylated and this tinguishes between methylated and non-methylated (CC which distinguishes between methylated and non-methylated (CC represent specifically claimed nucleotide sequences from the present cold invention. Oligonucleotides from the present invention can be used for disferentiating between healthy haematopoietic cells and proliferative convention. Oligonucleotides from the present invention can be used for convention. Oligonucleotides from the present invention can be used for disferentiating between healthy haematopoietic cells have acute for coldiferentiating between and acute myslogenous leukaemia, as probes for determining the cytosine methylation state and/or single nucleotide collymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA
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                                                                                                                                                                                                                                                                                                                                                                Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berlin K, Braun A, Distler J,
Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (x) for diagi
                                                                                                                                                                                                                                                                                                                                Claim 28; SEQ ID NO 342; 117pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haematopoietic cell proliferation disorder related DNA sequence
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72.5%;
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P, Grabs
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RESULT 12
ABL32304/c
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Matches 24
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL32304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders allowing for improved and informed treatment of patients
                                                                                                           including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelo: leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                              genes which
                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 277; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL32304
                                                                    Sequence 6309
                                                                                                                                                                                                                                     can
                                                                                                                                                                                                                                                                                    The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-)
                                                                                                                                                                                                                                es which are modified by the methylation of cytosines. The sequence be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                                                                                                                                                                    cid comprising and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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2000DE-01043826
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                                                                    BP; 1758 A; 69 C; 1364 G; 3118 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              system disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.0%;
85.7%;
54.0%;
75.0%;
                                                                                                                                                                                                                                                                                    provides a number of human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6309
                                                                                                                                                                                                                                                                                                                                                                                                    fragment of chemically modified gene, useful of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Pred. No. 1
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21.6;
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. 1.7e+02;
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RESULT 14 ADE84196/c

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RESULT 13
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                                               Ś
                                                                                                                                                                                                                                                                                  The invention relates to a novel method for detecting and differentiating competitions are colon cell proliferative disorders associated with at least one competition of the method comprises contacting a target concleic acid in a biological sample obtained from the subject with at competition are reagent or a series of reagents, where the reagent or series of reagents, distinguishes between methylated and non methylated CpG dinucleotides within the target nucleic acid. The molecules of the convention demonstrate cytostatic activity whilst the method may useful for detecting and differentiating between colon cell proliferative disorders, including cancers such as colon adenoma and colon carcinoma. The PNA (peptide nucleic acid)-oligomers are useful as probes for determining cytosine methylation state or single nucleotide colon carcinoma. The current sequence is that of the pretreated genomic DNA cregion of the invention. This sequence is not shown within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local :
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Rujan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 32; SEQ ID NO 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-731620/69
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                                                                                                                                                                                                             Sequence
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                                                                                                                                  Similarity
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AAACCTAACCCCAAACAATCCATCCTAC 3056
                                                 ATACCTACTCCCAAACAATCCATCTTAC
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Schmitt A;
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                                                                                                      Conservative
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                                                                                                                                                                                                                                                                    but
                                                                                                                                                                                                             BP; 1818 A; 0
                                                                                                                                                                                                                                                                    is taken
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85.7%;
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Pred. No. 1.7e
0; Mismatches
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                                                                                                                                                                                                                C; 1721 G; 3571 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                  Wipoweb.
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                                                                                                                                                        Length 7110;
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ADE84196 standard; DNA; 7110 BP.

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                                                                                                                                                      The invention relates to a method of detecting and differentiating CC between lymphoid cell proliferative disorders associated with at least CC one gene and/or their regulatory regions in a subject by contacting at CC target nucleic acid in a biological sample obtained from the subject with CC at least one reagent or series of reagents that distinguish between CC methylated and non-methylated CG dinucleotides within the target nucleic CC acid. The genes and/or their regulatory regions are preferably selected CC from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, MYOD1, CDH3, CC MYCL1, ELK1, ABL1, APC, BC12, CDH1, CDKN1A, CDKN1B, CDKN2A, CDKN2B, FOS, CC GSTPD1, HIC-1, MGMT, MLH1, MOS, MYC, PYEN, RB12, TGFBR2, TP73, CDKNIC, CC GSTAbeta, ESR1, APAF1, BAK1, BAX or HOXAS, Oligomers, peptide nucleic caid (PNA)-oligomers and/or isolated nucleic acids based on the sequences CC of the genes are useful for detecting the methylation state of all the CC Godinucleotides within one or more the sequences, or their complements, CC for determining the cytosine methylation state and or single nucleotide CC godinucleotides within one or more the sequences, or their complements, CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma, CC chronic lymphocytic leukenia, small lymphocytic lymphoma and follicular CC differentiation between subclasses, diagnosis, prognosis, treating and/or monitoring of lymphoid cell proliferative disorder. This sequence CC above mentioned genes.
                                                            Query Match
Best Local S
Matches 24
                                                                                                                                                 Sequence 7110 BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least one reagent that distinguishes between methylated and non-methylated CpG
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28-DEC-2001; 2001DE-01064501.
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methylated CpG dinucleotide; single nucleotide polymor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lymphoid cell proliferative disorder gene derived DNA #132. 1987 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burger M,
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4 ATACCTACTCCCAAACCAATCCATCTTAC 31
                                                                                  Similarity
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                                                            Conservative
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85.7%;
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                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lymphocytic lymphoma;
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Matches 24
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                                                                                                                                                    4 ATACCTACTCCCAAACAATCCATCTTAC 31
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The invention relates to a novel method for predicting the responsiveness co of a subject with a cell proliferative disorder of the breast tissues to a therapy comprising analysing the methylation pattern of a target nucleic acid by contacting at least one of the target nucleic acids in a biological sample obtained from the subject prior to or during treatment. The method of the invention has cytostatic activity, and may have a use in gene therapy. The set of oligonucleotides comprising at least two of the oligomers are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SURs) within the sequences. The methods, nucleic acid, oligonucleotide, and kit are useful for the treatment, characterisation, classification and/or differentiation, of treatment, characterisation, classification and/or differentiation, of predicting the responsiveness of a subject with a cell proliferative disorders. The method is also useful for predicting the responsiveness of a subject with a cell proliferative disorders. The method is also useful for the breast tissues to a therapy. The present sequence is used in the examplification of the breast tissues to a therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Foekens J, n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Predicting responsiveness of a subject with breast cell proliferative disorder, useful for treating or differentiating breast cell proliferative disorders comprises analyzing methylation pattern of a genomic DNA from the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 596; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002; 2002DE-01045779
07-JAN-2003; 2003DE-01000096
17-APR-2003; 2003DE-01017955
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Schmitt
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Schmitt M, Look MP,
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Marx A;
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Search completed: March Job time : 26.619 secs 5 2006, 18:11:42

ANACCTAACCCCAAACAATCCATCCTAC 3056

Conservative

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54.0%; 85.7%;

Score 21.6; D Pred. No. 1.7e 0; Mismatches

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Title:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                             Score
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Match
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Gapop 10.0 , Gapext 1.0
 41078325 seqs, 23393541228 residues
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CO117589
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CL084441	· CG383910	CZ727957	CG811817	CK949745	BM027586	AI382034	BF601210	AI467879	AA725064	AI698201	AI206216	CN317130	CK871857	CK864514	DT054853	BB264116	CL058859	CR818130 GR0AAA43D	AW687128 NF006C08R	AZ400686	CR843905	BZ173201
	) OGZAP61TV	OC Ba005	FSAAM35TR	4074916	GIT000109	te33g05.x	266128 MA	tj78e09.x	ai06h07	wa67g11.x	qr27f06.x	AGENCOURT	AGENCOURT	AGENCOURT	AGENCOURT	BB264116	CH216-88P	GROAAA	NF006C0	1M0167P01	GROAAA79A	CH230-369

# ALIGNMENTS

Query Match Best Local Matches 4	FEATURES SOURCE	AUTHORS TITLE JOURNAL COMMENT	RESULT 1 CC655939/c LOCUS LOCUS DEFINITION ACCESSION VERSION KEYMORDS SOURCE ORGANISM REFERENCE
'Match 100.0%; Score 40; DB 9; Length 687; Local Similarity 100.0%; Pred. No. 4e-05; Les 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-6043 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TF Class: metbylation filtered. Location/Qualifiers 1. 687 /organism="Zea mays" /organism="Zea mays" /fortain="genomic DNA" /strain="873" /db xref='taxon:4577" /clone="Zentered.etg." /clone="ib="ZM 0.7 1.5 KB" /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Renick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002) Other GSSs: OGWDQ20TM Contact: Cathy Whitelaw TIGR	CC656939  CC656939  CC656939  CC656939  CC656939  CC656939  CG56939  CG56939  CG56939  CG56939  CG566939  CG566939

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1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40

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AUTHORS
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CC656933
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                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 963)

1 (bases 1 to 963)

Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R. W., Nunberg, A., Robbins, D. and Lakey, N. Citek, R. W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
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Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize
Unpublished (2002)
Other_GSSs: OGIAGO8TH
                                                                                                                                                                                                                                        genomic survey sequence CC656933 CC656933.1 GI:32060225
                                                                                                                                                                                                                                                                           OGWDQ20TM ZM_0.7_1.5_KB genomic survey sequence.
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1 (bases 1 to 915)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Rohlfing, T.,
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Location/Qualifiers
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/clone=1ib="ZM 0.7_1.5KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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genomic clone ZMMBMa0716B15
                                                                                                                                                                                                                                                                                              genomic clone ZMMBMa0554D15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 915;
                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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REFERENCE
AUTHORS
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CW324514
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JOURNAL
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           836 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                                Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 819 row: c column: 19
Seg primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lilioppida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 702)

1 (bases 1 to 702)

Bedell, J. A., Budiman, M.A., Nunberg, A., Citek, R. W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CW324514 702 bp DNA linear GSS 31-OCT-2004 104 819_11477203_148_35910_078 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11477203, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR
9712 Medical Cent
Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                   Orion Genomics, LLC
4041 Forest Park Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorghum bicolor (sorghum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: methylation filtered.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Bedell JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     15660154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorghum genome sequencing by methylation filtration PLOS Biol. 3 (1), e13 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CW324514.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martienssen,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="ZMMBMa0554D15"
/clone=1b="ZM 0.7 1.5 KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
prepared from purified nuclei was randomly sheared,
                                                                                                                             /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4577"
                                                         /clone_lib="Sorghum methylation filtered library (LibID:
                                                                                     /db_xref="taxon:4558"
/clone="11477203"
                                                                                                                                                                                                                 location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:55040702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 40; DB 9;
100.0%; Pred. No. 4.2e-05;
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Conservative

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74 AGGACACCTACTCCCAAACAATCCATGTTACCCATGCAAC 113
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sorghum bicolor (sorghum)

sorghum bicolor (sorghum)

sorghum bicolor (sorghum)

sorghum bicolor

sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

spermatophyta; Viridiplantae; Streptophyta; Poales; Poaceae; PACCAD

spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

[ bases 1 to 296]

[ bases 1 to 296]

[ clate, R. W., Robbins, D.,

sedell, J. A., Budiman, M. A., Nunberg, A., Citek, R. W., Robbins, D.,

Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,

McMenamy, J., Smith, M., Holeman, H., Roe, B. A., Wiley, G., Korf, I.F.,

Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J. A. and

Martienssen, R. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorghum genome sequencing by methylation filtration PLoS Biol. 3 (1), el3 (2005)
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                                                 AGGACACCTACTCCCAAACAATCCCATGTTACCCATGCAAC 282
                                                                                                              AGGATACCTACTCCCAAACAAT-CCATCTTACTCATGCAAC 40
                                                                                                                                                                                                                                                                                                                                                               /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincIII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligsted into HincII-digested pBCSK(-) vector and electroporated into B. coli cells. This is a way methylation filtered library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="Sorghum methylation filtered library (LibID: 04)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             row: m column: 16
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                                                                                                                                                                                                                                                     DB 10; Length
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                                                                                                                                                                                       Indels
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                                                                     RESULT 7
BZ706605/c
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KEYWORDS
SOURCE
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H24137
LOCUS
DEFINITION
    ACCESSION
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 28
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                                                                                                                                                                                                                                                                                 346 AAATCTACTCTCAAACATTTCATCTTATACATGCA
BZ706605 375 bp D
SW41681-G07_55_13.ab1 Spider Monkey
geoffroyi genomic, genomic survey se
BZ706605
                                                                                                                                                                                                                                                                                                                              4 ATACCTACTCCCAAACAATCCATCTTACTCATGCA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
Insert Size: 1161
High quality sequence stops: 349
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@inage.llnl.gov) for further information.
Insert Length: 1161 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.

1 (bases 1 to 528)

1 (bases 1 to 528)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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ym50g08.rl Soares infant brain 1NIB Homo sapiens cDNA clone
IMAGE:51939 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 349.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="73 days post natal"
//lab_nost="DH10B (ampicillin resistant)"
//lab_nost="DH10B (ampicillin resistant)"
//lab_nost="DH10B (ampicillin resistant)"
//lab_nost="DH10B (ampicillin resistant)"
//lab_nost="DH10B (ampicillin resistant)
/
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/mol_type="mRNA"
/db_xref="GDB:424875"
/db_xref="taxon:9606"
/clone="IMAGE:51939"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                            'Score 23.8; DB 8;
Pred. No. 1.2e+02;
0; Mismatches 7;
                                                             ONA linear GSS 18-MAY-2003 genomic BAC library Ateles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 528;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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TITLE
JOURNAL
PUBMED
COMMENT

Contact: Bedell JA

Genomics,

FEATURES

Seq primer: k Reverse Class: methylation filtered

quali

ty sequence stop: 296.

Plate: fsbb001f170

Email: jbedell@oriongenomics.com

Forest Park Ave, St. Louis, 314 615 6979 314 615 5975

source

/organism="Sorghum bicolor" /mol\_type="genomic DNA" /cultivar="ATX623" /db\_xref="taxon:4558"

db\_xref="taxon:4558" clone="fsbb001f170m16"

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242 ۲ ORIGIN

Query Match Best Local S Matches 37

l Similarity 37; Conser

Conservative

0;

60.5%;

Score 24.2; D Pred. No. 75; 0; Mismatches

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REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS

CW445575.1

GI:55193536

SOURCE ORGANISM

RESULT 5 CW445575 LOCUS

DEFINITION

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                                                                                                                                                                                                                                                                                                                                                                                                                          255 GGATATCTACTTGTGAACCATACATTTTACTNAAGCAAC 217
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tu
Tel: 520 626 9595
Fax: 520 621 1259
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GR_EBO1H15.r GR_Eb Goss
mRNA sequence.
CO117589
CO117589.1 GI:48816276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qian,Y., Jin,L. and Su,B.

Construction and characterization of bacterial artificial chromosome library of black-handed spider monkey (Ateles geoffroyi)
Genome 47 (2), 239-245 (2004)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
Cebidae; Atelinae; Ateles.
1 (bases 1 to 375)
                                                                                                                                     2 GGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kettering Lab, 3223 Eden Ave.,
Tel: 1-513-558-6678
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GSS.
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                                                                                                        Global assembly of Cotton
                                                                                                                                                                                                                                                  Gossypium raimondii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clome_lib="Spider Monkey genomic BAC library" /note="Vector: pBACe3.6; Site 1: EcoRI; Genomic partially digested with EcoRI_ Vector pBACe3.6, Recombinants were transformed into DH10B. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Fibroblast"
/cell_line="AG05352"
/dev_stage="3_DA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
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/db_xref="taxon:9509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Ateles geoffroyi"
/mol_type="genomic DNA"
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Gossypium
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Pred. No. 1.4e+02;
0; Mismatches 10;
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                                 85721-0036, USA
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             ISB1-51D14_Sp6.1 ]
genomic survey sec
CL109241
CL109241.1 GI:406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CR181951. GI:49960800 GSS; genome survey sequence; MICER. Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR181951 783 bp DNA linear GSS 06-JUL-20 Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN361p21, genomic survey sequence.
                                                               CL109241
ISB1-51D14_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams, D.J., Biggs, P.J., Cox, A.V., Jonkers, J., Smith, J., Plumb, R.W., Rogers, J. and Bradley, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/dev_grage="3 to +3 DPA"
/lab_host="JH10B" +
/clone_lib="GR_Eb"
/clone_lib="GR_Eb"
/note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
EcoRV; Library made by Invitrogen wIth RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80.
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/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_Eb01H15"
                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN361p21"
/clone_lib="MHPN"
                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                  GI:40602876
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77.8%;
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.2e+02;
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Nishijima,I., Yu,Y.,
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                                                                  r GSS
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Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
Gasterosteus aculeatus
Craniata; Vertebrat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD495749 INDEX. 1253 bp mRNA linear EST 12-JUN-2003 CDA18-D05.yld-s SHGC-CDA Gasterosteus aculeatus cDNA clone CDA18-D05 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 TACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                                                                                   HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanfor
Tel: 650 725 5954
Fax: 650 725 7739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kingsley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.
Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2003)
                                                                                                                     High quality sequence start: 15
High quality sequence stop: 667.
Location/Qualifiers
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Kremitzki, C., Carter
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Xenopus tropicalis
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Acanthomorpha; Acanthopterygii; Percomorpha;
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Actinopterygii; Neopterygii; Teleostei; Euteleostei
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
                                                                                                                                                                                                                               Plate: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kingsley, DM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               physical map of the xenopus tropicalis genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,E. and Wilson,R.
                                                                                                                                                                                                                                                     kingsley@cmgm.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="txorn:8844"
/clone="ISB1-51D14"
/clone_lib="ISB1"
/clone_lib="ISB1"
/clone_"Vector: pBeloBAC11; ISB-1 Xenopus tropicalis
Library Segment 1"
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Salinas river, CA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to 1253)
                                                                                                      .1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carter, J., McPherson, J., Warren, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23.2; DB 10;
Pred. No. 2.3e+02;
D; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                             Stanford, CA 94305-5329, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gasterosteiformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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AUTHORS
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KEYWORDS
SOURCE
ORGANISM
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AZ883408/c
LOCUS
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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ883408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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were inserted In to the ZAP express vector unidirectionally in the sense orientation with respect to the lacZ promoter of pBK-CMV. An amplified library was prepared from approximately 3 million primary clones in the lambda ZAP Express vector. In vivo excision was then used to generate individual pBK-CMV phagemid clones for EST sequencing."
                                                                                                                                                                                                                                                                                                                                                                      /note="Tyector: lambda ZAP Express/pBK-CMV; Site_1: Such /note="Tyector: lambda ZAP Express/pBK-CMV; Site_2: XhoI (3' linker primer); The mixed organ cDNA library was generated using the ZAP-CDNA method by Stratagene. First strand cDNA synthesis was primed with a 50 bp linker primer containing an oligo of sequence preceeded by a synthesito XhoI site. 5 prime adaptors were used containing an EcoRI cohesive end. The finished cDNAs were inserted in to the ZAP express vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="mixed male and female"
tissue_type="heads and inte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:69293"
clone="CDA18-D05"
                                  58.0%;
Score 23.2; DB 6; Length 1253;
Pred. No. 2.4e+02;
0; Mismatches 8; Indels 0
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1047 TACCTCTTTCCCAACAATCCATCTTCACCATCCAAC 1082
AZ883408 405
RPCI-23-189L2.TJ RPCI-23 Mus
bp DNA
              DNA
genomic
linear
mic clone
 GSS 05-MAR-2001
RPCI-23-189L2,
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0; Gaps

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Mekaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi, Muroidea; Muridae; Murinae; Musi
Other_GSSs: RPCI-23-189L2.TV
                         Unpublished (1999)
                                                                  Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Kingo, P., and Fraser, C.M.
                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                        AZ883408.1 GI:13202353
                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence
                                                      Mouse BAC
                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                               End Sequences from Library RPCI-23
                                                                                                      Geer, K., Krol, M.,
                                                                                                         de
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Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pde)ongemail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bappac/orderingframe.htm). BAC end page: http://www.thori.org/bappac/orderingframe.htm). BAC end Plate: 189 row: L column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                          Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                  mail: szhao@tigr.org
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="RPCI-23-189L2"
                                                                                                                                                                               ocat
                                                                                                                                                                            on/Qualifiers
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'sex="Female"

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ACCESSION
VERSION
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CJ037346
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                                         Matches
                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                              Best
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                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
                                       l Similarity
29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STARF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEDE (Pig EST Data Explorer): construction of a derived from porcine full-length cDNA libraries Nucleic Acids Res. 32 (1), D484-D488 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CJ037346 full-length enriched swine cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 Ikenodai, Tsukuba,
Tel: +81-29-838-8627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Okumura,N., Hamasima,N. and Awata,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sus.
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                                                                                                                                                                                                                                                                                                                                                                                Vector sequences were eliminated by RepeatMasker version 2002/07/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Hirohide Uenishi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (pig)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          scrofa cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGTAACAAATCCCAAACATGTCTTCTTAGTCATGCAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 662)
                                                                                                                                                                                                                                                                                                                      quality bases were trimmed Location/Qualifiers
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                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
//lab_host="DH10B"
//clone lib="RPCI-23"
/clone lib="RPCI-23"
/clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_and/or brain genomIc DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into bH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                        /tissue type="testis"
/dev_stage="adult"
/clone_lib="full-length
testis"
                                                                                                                                                                                                                                        /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                         1. .662
                                                                                                                                                                                                                       clone="TES01G080111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.5%;
74.4%;
                                                        57.5%;
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Pred. No. 2.4e=
0; Mismatches
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                                     Score 23; DB ?
Pred. No. 2.6e-
0; Mismatches
                                       0;
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                                                                                                                                                             enriched swine
                                                                               DB 7;
                                                            .6e+02;
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                                                                           Length 662;
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                                         Indels
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                                                                                                                                                             CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 database
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adult testis Sus
                                       ٥,
                                                                                                                                                             library,
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CJ035837
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                                                                                           KEYWORDS
                                                                                                             VERSION
                                                                                                                                                                 DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
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                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                  609
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CJ035837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,N., Hamasima,N. and Awata,T.
PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
Nuclic Acids Res. 32 (1), D484-D488 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (pig)
                                                                                                                                                           BG506830 798 bp n
601861443F1 NIH_MGC_77 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Animal Genome Laboratory, Genome Research Department National Institute of Agrobiological Sciences 2 Ikenodai, Teukuba, Ibaraki 305-8602, Japan Tel: +81-29-838-8627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CJ035837 full-length enriched swine cDNA library, scrofa cDNA clone TES01E060090 5', mRNA sequence.
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                      Homo sapiens
                                                                                                                            BG506830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Hirohide Uenishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Hominidae; Homo.
                                                                      Homo sapiens (human)
                                                                                                             BG506830.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vector sequences were eliminated by RepeatMasker version 2002/07/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14681463
                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              crossmatch version 0.990319 quality bases were trimmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 790)
                                                                                                                                                  sequence.
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="full-length enriched swine cDNA library, adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="TES01E060090"
/tissue_type="testis"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Sus scrofa"
|mol_type="mRNA"
                                                                                                             GI:13468347
                                                                                                                                                                                                                                                                                                                                                                        57.5%;
                                                                                                                                                                                                                                                                                                                                                        <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                        Score 23; DB 7;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  790
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swine cDNA library,
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                                                                                                                                                                 mRNA line
s cDNA clone
                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                            Length 790;
                                                                                                                                                                                                                                                                                  647
                                                                                                                                                                     IMAGE: 4071154 5',
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adult testis
                                                                                                                                                                                       EST 27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                        0,
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Search completed: March 6, 2006, 01:57:49 
Job time : 188.843 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.5%; Score 23; DB 2; Length 798; Best Local Similarity 83.9%; Pred. No. 2.7e+02; Matches 26; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                       222 ACTCCCAAACCAGCCTTCTTAGTCATGCATC 192
                                                                                                                                                                                                                                                                                     10 ACTCCCAAACAATCCATCTTACTCATGCAAC 40
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Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 798)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Clone distribution: MGC clone distr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 798
//organism="Homo sapiens"
/mol_type="mRVA"
/db_xref='taxon:9606"
/db_xref='taxon:9606"
/db_mref='taxon:9606"
/clone='IMAGE 4707154"
/lab_host="MMGE 4707154"
/clone_lib="NHH_MGC_77"
/clone_lib="NHH_MGC_77"
/clone_lib="NHH_MGC_77"
/fote="Dorgan: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgctcggcc); Site 2: SfiI (ggccattatggcc); Site 3: Afil (ggccattatggcc); Afil (ggccattatggcc);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLCM916 row: e column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, or G and N = A, C, G, or T). Average insert size 1.9 tb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ity sequence stop: 2.
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 2000000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         March 5, 2006, 21:54:12; Search time 11.1834 Seconds (without alignments) 6357.883 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-
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19.6	19.6	19.6	19.6	19.6	19.6	9	9	19.6	9	9	9	19.6	9	9	19.8	٥	٠	19.8		19.8	•
49.0	49.0	49.0	49.0	49.0	49.0	49.0	49.0	49.0		49.0			49.0	49.5	49.5	49.5			9		
140315	107937	89892	80859	80858	75480	66986	6330	4322	964	601	601		189	265038	74097	74096	9366	2971	2046	1164	
w	w	ω	ω	w	ω	ω	w	N	ω	w	w	ω	w	w	w	w	w	w	ω	ω	
US-09-949-016-14141	US-09-949-016-17192	US-09-949-016-13667	US-09-949-016-15715	US-09-949-016-12659	US-09-949-016-16090	US-09-596-002-29	US-09-949-016-15506	US-08-537-342-1	US-09-775-398-26	US-09-949-002-4265	US-09-949-016-83111	US-09-949-016-83110	US-09-540-236-1562	US-09-949-016-15779	US-09-949-016-16239	US-09-949-016-11785	US-09-949-016-17437	US-09-710-279-3449	US-09-248-796A-6906	US-09-134-001C-2534	
Sequence 14141, 1	Sequence 17192, 1	Sequence 13667, 1	Sequence 15715, 1	Sequence 12659, 1	Sequence 16090, 1	Sequence 29, App.	Sequence 15506, 1	Sequence 1, Appli	Sequence 26, Appl	Sequence 4265, Ap	Sequence 83111, 1	83110,	Sequence 1562, Ap	Sequence 15779, 1	Sequence 16239, 1	Sequence 11785, I	17437,	Sequence 3449, Ap	Sequence 6906, Ap	Sequence 2534, Ap	

### ALIGNMENTS

GENERAL INFORMATION: APPLICANT: Albert

Marc C.

880-499-1

Application US/08880499

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US-08-880-499-1
Query Match
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TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: Patentin Release #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880
FILING DATE: CONCURRENTLY HER
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION.
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REGERENCE/DOCKET NUMBER: 0578
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STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy d
                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LICANT: Huffman, Gary A.
JICANT: Kendall, Timmy L.
JICANT: HUFFMAN L.
JICANT: KENDALL
JI
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CONCURRENTLY HEREWITH
                                                                                                                                                    DNA (genomic)
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                                                                                                                                                                                                                                                        single
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100.0%; Score 40;
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RESULT 2
US-08-880-499-2
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                                                                                                                                                                                                                                                                                                                  RESULT 3
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, P
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
ATTORNEY/AFRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08880499 Patent No. 6037523
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                                                                                                                                                                                                     Sequence 7790, Application US/09949002
Patent No. 6900016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (general control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Townston
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ZIP: 50131
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STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                            1239
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Box 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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100.0%; Pr
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Pred. No. 6e-
0; Mismatches
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; Mismatches
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6e-07;
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                                                                 DISEASE, METHODS OF DETECTION
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; TYPE: DNA
; ORGANISM: Human
US-09-949-002-7790
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; ORGANISM: Human
US-09-949-002-7791
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US-09-248-796A-5546
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US-09-248-796A-5546
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CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/331,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7790
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FAST-SEQ for Windows Version 4.0
SEQ ID NO 7791
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, N
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
CURRENT FILING DATE: 2000-01-28
                                                                                                                                                                                                                                                                                                                             Sequence 5546, Application No. 6747137
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                              NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 5546
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                                                                                                                     APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PELING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
               LENGTH: 1071
TYPE: DNA
ORGANISM: Candida albicans
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74.3%;
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); Mismatches
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Pred. No. 51;
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Pred. No. 51;
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US-09-949-002-782/c
                                                                                                                                   ; ORGANISM: Human
US-09-949-016-14995
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                                                                                                                                                                                                      SOFTWARE: Fast
SEQ ID NO 14995
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APPLICANT: VENTER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14995, Application US/09949016
Patent No. 6812339
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SEQ ID NO 782
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CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/231,401 PRIOR FILING DATE: 2000-09-08
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TILE OF INVENTION: WITH INVELAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION YILL OF INVENTION: AND USES THEREOF
TLE REFERENCE: CL000790
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TLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                          ENGTH:
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les 26; Conservative
                                                                  Local Similarity 85.
 31591 ATTCCTACCCACAAACCATCCATCTTA 31565
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                               4 ATACCTACTCCCAAACAATCCATCTTA 30
                                                                                                                                                                                        42075
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                                                                                51.5%;
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                                                                  0; Mismatches
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                                                                                    Score 20.6; DB 3
Pred. No. 1.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20.6; DB 3; Length 14882; Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                    DB 3; Length 42075;
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                                                                  Indels 0;
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                                                 ; NAME/KEY: CDS
; LOCATION: (231)..(749)
US-09-774-528-184
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Query Match
Best Local Similarity
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Patent No. 681
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                                                                                                                                                                   SOFTWARE: pt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·09-949-016-65770/c
                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-774-528-184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20
                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                        FEATURE:
                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                             TLE OF INVENTION:
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                                                                                                                                                                                                                                                             REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184,
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                                                                                                                                                                                                                                                                                          Drmanac, Radoje T.
INVENTION: No. 6743619el Nucleic Acids and
                                                                                                                                                                                      pt_FL_genes Version 2.0
                                                                                                                                                                                                                                                                                                                          Wehrman, Tom
Wang, Jian-Rui
Wang, Dunrui
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ıdi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                              Feiyan
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Ryle
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Yonghong
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                                                                                                                                                                                                                                                                   No. 6743b19c.
Polypeptides
 51.0%;
71.1%;
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Pred. No. 61
 Score 20.4;
Pred. No. 68;
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                 Length 973;
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RESULT 11
US-08-945-056-4
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Best Local Similarity
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APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6919193el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802CON
CURRENT APPLICATION NUMBER: US/10/120,988
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 09/774,528
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tang, Y. rom
APPLICANT: Goodrich, Ryle
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (231)..(749)
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Coupland, GAPPLICANT: Putterill,
                                                  CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               APPLICATION NUMBER: PCT/GB95/02561 FILING DATE: 01-NOV-1995
                                                                                         APPLICATION NUMBER: FILING DATE: 20-OCT
                                                                                                                                                                                                                                                                              STREET: 8th Floc
                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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   APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
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                                                                                                                                                                                                                                     Virginia
7: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu, Chenghua
Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/10120988
                                                                                                                                                                                                                                                                                             E: Nixon & Vanderhye PC
8th Floor, 1100 No. 6077994th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                         Genetic control of flowering
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71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                              George M.
                                                                                                            US/08/945,056
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                                  RESULT 13
US-09-949-016-17420
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                                                                                                                                                                                                                                                          ; FEATURE:
; LOCATION: misc feature
; LOCATION: (1)...(51770)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13668
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Sequence 17420, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13668
LENGTH: 51770
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Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                      Matches
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 816-4000 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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STRAIN: Landsberg erecta
POSITION IN GENOME:
MAP POSITION: Chromosom-
-945-056-4
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 62
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 02-NO
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                                                                                                                                                                                                      Local
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                                                                                                              9851 GGATTCCTGGGCTCAAGCAATCCTCCTGCCTCAGGCAA 9814
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                                                                                                                                             2 GGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
                                                                                                                                                                                    Similarity 71.1
27; Conservative
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71.1%;
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Pred. No. 92;
                                                                                                                                                                                    Score 20.4; DB 3;
Pred. No. 1.6e+02;
0; Mismatches 11;
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Length 51770;

Indels

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Length 4201;

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Indels

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Gaps

THE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
THE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF,

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Best Local Similarity 71.1
Matches 27; Conservative
                                                                                                Query Match
Best Local
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Patent No. 68123:
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: VENTER, J. Craig et al.

ITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

ITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                       AME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: n = A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AME/KEY: misc_feature
OCATION: (1)...(84571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JRRENT APPLICATION NUMBER: US/09/949,016
JRRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                            GANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 84571
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53133 GGAAATCAACTCCAAAAAGGAACCTTCAAAATCATGCAA 53096
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                                                                                                                                                                                                                                                                                                          NO 1182
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                                                                                                                                                                    INFORMATION: n = A, T, C or G
                                                                      l Similarity 71.1
27; Conservative
                                                                                                                                                                                                                                                                                    126200
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                                   GGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATION NUMBER: US/09/949,016
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71.1%;
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                                                                                       Score 20.4; DB 3; Length 126200; Pred. No. 1.9e+02;
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Pred. No. 1.7e+02;
0; Mismatches 11; Indels 0;
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                                                      Query Match 51.0
Best Local Similarity 71.1
Matches 27; Conservative
                                                                                                                                             OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                              VAME/KEY: misc_feature
53133 GGAAATCAACTCCAAAAGGAACCTTCAAAATCATGCAA 53096
                            2 GGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
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OLYMORPHISMS IN KNOWN GENES ASSOCIATED
OTHER PROPERTION AND USES THEREOF
                                                          51.0%; Score 20.4;
71.1%; Pred. No. 1.
tive 0; Mismatche
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                                                              Mismatches
                                                                                            DB 3;
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Search completed: March 5, 2006, 22:36:28
Job time : 11.1834 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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1: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/US09A PUBCOMB.seq:*

3: /cgn2 6/ptodata/1/pubpna/US09A PUBCOMB.seq:*

4: /cgn2 6/ptodata/1/pubpna/US09B PUBCOMB.seq:*

5: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2 6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

8: /cgn2 6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

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  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
US-10-713-381-1

US-10-713-381-2

US-10-719-99-6800

US-10-424-599-31006

US-09-925-065A-70302

US-10-424-599-83179

US-10-424-599-83179

US-10-424-599-83179

US-10-925-065A-591011

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US-09-925-065A-393490

US-09-925-065A-393490

US-10-473-126-342

US-09-925-065A-281837

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US-10-713-381-5
US-10-713-381-3
US-10-713-381-9
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                                        Sequence 6, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 20, Appli
Sequence 31006, Ap
Sequence 670302,
Sequence 670302,
Sequence 1948, Ap
Sequence 591012,
Sequence 591013,
Sequence 591013,
Sequence 591013,
Sequence 591013,
Sequence 25177,
Sequence 3912,
Sequence 3912,
Sequence 3913,
Sequence 3913,
Sequence 3913,
Sequence 3914, App
Sequence 377, App
Sequence 377, App
Sequence 31837,
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Sequence 1568, Ap	Sequence 344, App	Sequence 198, App	•	Sequence 361, App	Sequence 2594, Ap	Sequence 20320, A	Sequence 937247,	Sequence 285328,	Sequence 285327,	Sequence 285326,	Sequence 24043, A	Sequence 2, Appli	Sequence 1, Appli	Sequence 2335, Ap	Sequence 23, Appl	Sequence 901, App	Sequence 4, Appli	Sequence 128, App	Sequence 1555, Ap	Sequence 1555, Ap	Sequence 63167, A	

#### ALIGNMENTS

Sequence 6, Application US/10713381 Publication No. US20040221331A1 GENERAL INFORMATION:

```
APPLICANT: HOFMAN, MARC C.
APPLICANT: APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 1997-06-23
RUMBER OF SEQ ID NOS: 24
SOFTMARE: PATENTIN PATENTIN SECONDATE: 1997-06-23
RUMBER OF SEQ ID NOS: 24
SOFTMARE: PATENTIN VET. 2.0
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 40
TYPE: DNA
ORGANISM: Zea mays
US-10-713-381-6
                                                                                                                                                                                                                                                                                  RESULT 2
US-10-713-381-5
Sequence 5, Application US/10713381

Sequence 5, Application US/10713381

Publication No. US20040221331A1

GENERAL INFORMATION:

APPLICANT: ALBERTSEN, MARC C.
APPLICANT: GARNAT, CARL W.
APPLICANT: GARNAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.

TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 40
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CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24

FILE REFERENCE: 578R

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-5
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US-10-713-381-3
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Best Local Similarity
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Best Local :
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Publication No. US20040221331A1
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARWART, CARL W.
APPLICANT: HUFFMAN, GARY
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
                                                                         APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
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APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                              APPLICANT: ALBERTSEN, MARC C. APPLICANT: FOX, TIMOTHY W.
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); Mismatches 0;
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; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-9
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US-10-713-381-1
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
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Publication No. US20040221331A1
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Best Local Similarity
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Publication No. US20040221331A1
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APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ALBERTSEN, MARC C. APPLICANT: FOX, TIMOTHY W. APPLICANT: GARNAAT, CARL W.
                                                                    CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                               APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNART, CARL W.
APPLICANT: HUPFMAN, GARY
APPLICANT: HUPFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1394
TYPE: DNA
ORGANISM: Zea mays
TYPE: DNA
                   ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1239 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
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                                                     PatentIn Ver. 2.0
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100.0%; Pred. No. 5.7e-06;
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Pred. No.
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US-10-719-993-6880/c
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US-10-713-381-2
                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_128002C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-424-599-31006
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Tocal Similarity
                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 31006
LENGTH: 706
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Best Local Similarity 84.4%;
Matches 27; Conservative
                                                                                   Query Match
Best Local S
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Publication No. US20040031072A1
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                                                                                                                                                                                                                                                                                                             APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55542
SOFTWARE: FRANKEQ for Windows Version 4.0
EQ ID NO 6880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001496
                                                                                                                                                                                          TYPE: DNA ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equence 6880, Application US/10719993
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PPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(85779)
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RGANISM: Homo sapiens
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5 TACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                      Similarity
                                                                58.0%;
ilarity 77.8%;
Conservative
                                                              0; Mismatches
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Pred. No. 39
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                                                                                                    DB 7; Length 706;
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226 ATACCTGGTCCCATACACTCCATCTTACT 254

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US-10-425-115-143168
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US-10-425-115-143168
                                                  Query Match
Best Local S
Matches 25
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                                                                                                                                                                                                                        SEQ ID NO 143168
LENGTH: 294
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Publication No. U
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Best Local
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                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2003-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
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CURRENT FILING DATE: 2001-08-08
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                                                                                                                                                                              TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT: Zhou,
                                                                                                                                                                 FEATURE:
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4 ATACCTACTCCCAAACAATCCATCTTACT 32
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                                                                Similarity
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                                                  Conservative
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US20040214272A1
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                                                             56.5%;
86.2%;
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2003-04-28
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74.4%;
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                                              Score 22.6; D
Pred. No. 56;
0; Mismatches
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Pred. No.
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                                                                                    DB 8; Length 294;
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                                                                                                                         RESULT 13
US-09-925-065A-591011/c
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US-10-087-192-1948
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SEQ ID NO 1948
LENGTH: 226215
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LENGTH: 315
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                                                          Sequence 591011, Application US/09925065A publication No. US20050228172A9 ENERAL INFORMATION:
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Best Local
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Best Local
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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TITLE OF INVENTION: NOVEL COMPOSITIONS AND
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR TLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 2059
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APPLICANT: Engelhard, Eric
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: PAT_MRT3847_46127C.1
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                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
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72.5%;
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Pred. No. 69;
0; Mismatches
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Pred. No. 2.5e+02;
0; Mismatches 11
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RESULT 14
US-09-925-065A-591012/c
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; ORGANISM: Homo sapiens
US-09-925-065A-591012
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR TILING DATE: 2000-11-20
PRIOR PPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR PILIOR DATE: 2001-01-16
PRIOR PILIOR DATE: 2001-01-16
PRIOR PILIOR DATE: 2001-01-16
PRIOR PILIOR DATE: 2001-05-09
PRIOR PILIOR DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Huma
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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ORGANISM: Homo sapiens
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Pred. No. 94;
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Pred. No. 94;
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RESULT 15
US-09-925-065A-591013/c
; Sequence 591013, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:

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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: 108027.135

CURRENT APPLICATION NUMBER: US/09/925.065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR PRILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/251,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/289,846

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Database :
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Listing first 45 summaries
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_6/ptodata/2/pubpna/USO9_NEW_PUB.seq1:*
_6/ptodata/2/pubpna/USI0 NEW PUB.seq:*
_6/ptodata/2/pubpna/USI0 NEW PUB.seq:*
_6/ptodata/2/pubpna/USI1_NEW_PUB.seq:*
_6/ptodata/2/pubpna/USI1_NEW_PUB.seq2:*
_6/ptodata/2/pubpna/USI1_NEW_PUB.seq3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	В	ID	Description
0	23	57.5	636	٥ :	US-09-925-065A-670302	Sequence 670302,
N	22.6	56.5	3242	œ	US-10-750-185-58624	
w	22.6	56.5	3242	œ	US-10-750-623-58624	
C 4	22.2	55.5	611	თ	US-09-925-065A-591011	
ი 5	22.2	55.5	611	σ	US-09-925-065A-591012	
o 0	22.2	55.5	. 611	ά	US-09-925-065A-591013	
7	22.2	55.5	613	σ	US-09-925-065A-253727	
c 8	22	55.0	628	σ	US-09-925-065A-888321	
o 9	21.6	54.0	865	0	US-09-925-065A-393490	
10	21.4	53.5	560	6	US-09-925-065A-281837	
11	21.4	53.5	560	σ	US-09-925-065A-281838	
c 12	21.4	53.5	620	თ	US-09-925-065A-189248	
13	21.4	53.5	653	σ	US-09-925-065A-63167	
14	21	52.5	201	12	US-11-124-367A-24503	Sequence 24503, A
15	21	52.5	617	σ	US-09-925-065A-285326	Sequence 285326,
16	21	52.5	617	σ	US-09-925-065A-285327	Sequence 285327,
17	21	52.5	617	6	US-09-925-065A-285328	Sequence 285328,
c 18	21	52.5	653	σ	US-09-925-065A-937247	
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### ALIGNMENTS

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RESULT 2
US-10-750-185-58624
; Sequence 58624, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-05-9
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SEQ ID NO 670302
LENGTH: 636
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                    Query Match 57.5%; Score 23; DB 6; Length 636; Best Local Similarity 74.4%; Pred. No. 11;
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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RESULT 4
US-09-925-065A-591011/c
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; ORGANISM: Bovine
US-10-750-623-58624
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                                                      GENERAL INFORMATION:
                                                                       Sequence 591011, Application US/09925065A
Publication No. US20040181048A1
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Best Local Similarity
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Publication No. US20050287531A1
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILIOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
APPLICANT: Wang, David G. TITLE OF INVENTION: Ident TITLE OF INVENTION: Nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMII100-1
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
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75.7%;
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Pred. No. 23;
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US-09-925-065A-591012/c
; Sequence 591012, Application US/09925065A
; Publication No. US20040181048A1
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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                                                                                  Matches
                                                                                                          Query Match
Best Local
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US
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PRIOR APPLICATION NUMBER: US 60/250,092
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/261,766
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ORGANISM: Homo sapiens
                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
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351 CCAAACAAACCACCTTACTCATGCAGC 325
                      14 CCAAACAATCCATCTTACTCATGCAAC 40
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0; Mismatches
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Pred. No. 22;
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Pred. No. 22;
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RESULT 6
US-09-925-065A-591013/c
US-09-925-065A-591013, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:

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RESULT 8
US-09-925-065A-888321/c
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US-09-925-065A-591013
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ORGANISM: Homo sapiens
-09-925-065A-253727
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                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
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PRIOR FILING DATE: 2000-10-24
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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                                                              292 GAAATCAACTCCAAAASAAACCCTCAAAATCATGCA 328
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                                                                                           2 GGATACCTACTCCAAACAATCCATCTTACTCATGCA 38
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ON NUMBER: US 60/261,766
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Pred. No. 22;
1; Mismatches
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Pred. No. 22;
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Best Local :
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-393490
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US-09-925-065A-888321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
NITLE OF INVENTION: Nucleotide Polymorphisms in the Human
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                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/243,096
FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/261,766
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APPLICATION NUMBER: US 60/250,092
FILING DATE: 2000-11-30
228 TATCTSCTCTCAATCAATCCATCTTACT 201
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                                 5 TACCTACTCCCAAACAATCCATCTTACT 32
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85.7%;
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                                                                                           Score 21.6;
Pred. No. 38
                                                                         Mismatches
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                                                                                                           Length 598;
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RESULT 10 US-09-925-065A-281837

Sequence 281837, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:

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                                             Matches
                                                                                         Query Match
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Publication No. US20040181048A1
                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
-09-925-065A-281838
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Huma
FILE REFERENCE: 108827.135
FURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR APPLICATION NUMBER: US/09/243,096
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PRIOR APPLICATION NUMBER: US 60/289,846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 957086
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                                                                                                                                                                                                           ID NO 281838
ENGTH: 560
                                                                   Local
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28; Conserv
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  1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
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71.8%;
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Pred. No. 4
                                           Score 21.4; DB Pred. No. 46; O; Mismatches
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                                             11; Indels
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; ORGANISM: Homo sapiens
US-09-925-065A-189248
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US-09-925-065A-189248/c
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                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-63167
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                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
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Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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SEQ ID NO 189248
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Best Local
                    Query Match
Best Local Similarity
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
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PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
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PRIOR FILING DATE: 2000-11-30
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09
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                                                                                                                                   LENGTH:
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Pred. No. 47;
  Score
Pred.
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  No. 4
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186 AGGAAACCTACACCCTGACATGTCAACTAACTACTGCAA 224

1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39

28; Conservative

0; Mismatches 11; Indels

Gaps

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RESULT 15
US-09-925-065A-285326
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US-11-124-367A-24503
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US-11-124-367A-24503
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Best Local Similarity 73.0
Matches 27; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 285326, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                   ORGANISM: Homo sapiens
-09-925-065A-285326
                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08
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SENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR ETITING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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blication No. US20060024700A1
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                                                                                                                                                           ID NO 2
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LE OF INVENTION: Genetic Polymorphisms Associated with
LE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/582,609
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                                                                                                                                                                                                                 PLICATION NUMBER: US 60/289,846
PLICATION NUMBER: US 60/289,846
LING DATE: 2001-05-09
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NG DATE: 2005-05-09
                                                                                                                                                                                                                                                                                    ON NUMBER: US 60/261,766
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NTE: 2004-05-07
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73.0%;
Score 21; DB 6; Length 617; Pred. No. 68;
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Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps

Qy 4 ATACCTACTCCCAAACCATCTTACTCATGCAAC 40
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Search completed: March 6, 2006, 10:32:52 Job time : 42.7555 secs

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Maximum DB seq length: 2000000000
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157
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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BD062176
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20.6	20.6	20.6	20.6	20.6	20.6:	20.6	20.6	20.6	20.6	0.8	20.8	0.8	20.8	20.8	20.8	0.9	0.9	0.9	20.9	0.9	0.9	20.9	0.9	21.1	21.1	21.1	
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AC157998 Mus m	AC147437 Gallus ga	AC148229 Gallus ga	AL731779 Mouse	AC159811 Mus m	Continuation (	BC094506 Mus m			BC020027 Mus m	AC097405 Rattus	AC140696 Rattus	AC127012 Rattus	AL953855 Zebrafish	AC147308 Pan	AC099973 Mus	AC149044 Pan t	AC019229 Homo sapi	AC087485 Homo	Homo	AL121875 Human	4 Hom	Homo	AC103745 Homo	AC146134 Pan trogl	AC091864 Homo	AC011290 Homo	
muscu	s ga	us ga	DNA	muscu	(6 of	muscu	muscu	muscu	muscu	us no	us no	us no	fish	trogl	muscu	rogl	sapi	sapi	sapi	DNA	Ното варі	gapi	gapi	rogl	sapi	sapi	

# ALIGNMENTS .

AX224402  LOCUS  LOCUS  AX224402  DEFINITION  Sequence 9 from Patent W00160997.  ACCESSION  AX224402.1 GI:15554644  XEYWORDS  Cae mays  SOURCE  Zea mays  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea  REFERENCE  AUTHORS  Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.  TITLE  Male tissue-preferred regulatory region and method of using same patent; W0 0160997-A 9 23-AUG-2001;  Patent: W0 0160997-A 9 23-AUG-2001;  PORGANISH  Male tissue-preferred regulatory region and method of using same patent; W0 0160997-A 9 23-AUG-2001;  PATENTAL TORSER HI-BRD INTERNATIONAL, INC. (US)  FEATURES  FEATURES  OURGAL  AUTHORS  Location/Qualifiers  Ouery Match  1. 255;  Best Local Similarity 100.0%; Score 157; DB 6; Length 255;  Best Local Similarity 100.0%; Pred. No. 5.5e-40;  Best Local Similarity 100.0
GI:15554644  GI:15554644  GI:15554644  Viridiplantae; Streptophyta; Embryophyta; Tracta; Magnoliophyta; Liliopsida; Poales; Poacea Coidees; Andropogoneae; Zea.  C., Fox,T., Garnaat,C.W., Huffman,G. and K. Preferred regulatory region and method of us 0160997-A 9 23-AUG-2001; BEED INTERNATIONAL, INC. (US) Cation/Qualifiers 255 Seation/Qualifiers 257 100.0%; Score 157; DB 6; Length 255; 100.0%; Pred. No. 5.6e-40; 100.0%; Pred. No. 5.6e-40; 100.0%; Pred. No. 5.6e-40; 101.0%; Pred. No. 5.6e-40; 102.0%; Pred. No. 5.6e-40; 103.0%; Pred. No. 5.6e-40; 104.0%; Pred. No. 5.6e-40; 105.0%; Pred. No. 5.6e-40; 106.0%; Pred. No. 5.6e-40; 107.0%; Pred. No. 5.6e-40; 108.0%; Pred. No. 5.6e-40; 109.0%; Pred. No. 5.6e-40; 100.0%; Pred. No. 5.ee-40; 100.0%; Pred. No. 5.ee-40; 100.0%; Pred. No. 5.ee-40; 100.0%; Pred

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Patent: JP 2001520523-A 1 30-OCT-2001;

Put JP 2001520523-A 1 30-OCT-2001

Put JP 2001520523-A 1 30-OCT-2001

Put JP 2001520523-A 1 30-OCT-2001

Put JP 19-JUN-1998 JP 199504910

Put JP 19-JUN-1997 US 08/880499

Put MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFM POX CIZN15/B2, CIZN15/29, CIZN9/24, CIZN9/22, CIZN9/10, CIZN9/00 PC C CIZN15/B2, CIZN15/29, CIZN9/24, CIZN9/22, CIZN9/10, CIZN9/00 PC R0.145/00

CC Strandedness: Single;
CC Topology: Linear;
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Albertsen, M.C., Fox, T.W., Garnaat, C.W.,
Kendall, T.L.
                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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   Male tissue-preferred regulatory region Patent: JF 2001520523-A 2 30-OCT-2001; PIONEER HI BRED INTERNATIONAL INC PN JF 2001520523-A/2
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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19-JUN-1998 JP 1999504910
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MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMITIMMY L KENDALL
C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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i method of using same.
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F 19-JUN-1998 JP 1999504910

PR 23-JUN-1997 US 08/880499

PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUF

PI TIMMY L KENDALL.

PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00

CC C12N15/00

CC Strandedness: Single;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;
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AX224394
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Spermatophyta; Magnoliophyta; Liliopsida; Poalea; Poaceae; PACCAD
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CAACTTCCATGCAAACACGCACATATGTTTTCCTGAAC
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                                            AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
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/mol_type="unassigned
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Sequence 2 from
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Clade; Panicoideae; Andropogoneae; Zea.
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Eakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Sequence 3 from Patent WO0160997.
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AX224396.1 GI:15554638
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SRKDHJAILLEGEGTGBLLAYDEFTSGVHVKSUGRGGFWAVAIDCCTFPAGEVFAKEPMLR
RIMRYMLISGFRAGEVEVFANLFGFPDNVRSNGRGGFWAVAIDCCTFPAGEVFAKEVGSK
TLYKFPLSLKVLTMKKAARRHHTVLALLOGEGRVVEVLEDRGHEVMKLVSEVBEKE
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DGRVVRMMGEBAGWETFAVMNPDMSEBVCANGVNSTTRKQHEKBEBFCGRPLGILRFHGE
TGELYVADAYYGLMVVGQSGGVASSVARBADGDPIRFANDLDVHRNGSVFFTDTSNRY
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Pred. No. 2.1e-36;
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RESULT 8 APROBADO D86/c WPCOMMENT Sequence split into 362 fragments Locus Fragment Name Begin End APROBADO DO 1 100001 210000 APROBADO DO 2 200001 310000 APROBADO DO 3 00001 1110000 APROBADO DO 3 1000001 2010000 APROBADO DO 3 1000001 20100000 APROBADO DO 3 1000001 2010000 APROBADO DO 3 1000001 2010000001 201000000000000000	QY 120 GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
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/noce="(Japonica Cultivar-group)"  gene	CCTTGCCTATTCTCAACCAACAGANTACCTACTCCCAACAATCCATCTTACTCATGCAA 123 CCTTGCCTATTCCGAACCAACAGAACACCTACTCCCAAACAATCACCTCGACTCATGCAA 36303	AAGAGGATACCTAC                   AACAGAACACCTAC	CTATTCTGAACC	36362 CCTTG
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om/ or/ or/	DB 15; Length 110000;	Score 54; DI	34.4%;	y Match
Location/Qualifiers 1137327		19610000	19500001 19600001	P008209_195
nucleotide sequence of this BAC clone was generated by combining Syngenta, Monsanto and Arizona Genomics Institute sequencing data.		19410000 19510000	19300001	P008209_193 P008209_194
single subclone. Areas 69957-70761, 89836-90416, 98951-99009, 105316-105607, and 133052-133152 are covered by Monsanto only. The		19210000	19100001	P008209_191 P008209_192
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JOURNAL SUBMITTER (16-ARK-2003) CLEMBON UNIVERSITY GENORICS INSTITUTE, Clembon University, 100 Jordan Hall, Clembon, SC 29634, USA		18010000	18000001	1 1
		17910000	17800001	J. J.
AUTHORS WING, K.A., IU, I., SOMETIMIA, C., CHEM, M., ALM, M., FRANKO, L., ALM, M., FRANKO, L., Thurmond, S.K. and Cum. C.		17710000	1760001	P008209_176
5 (bases 1 to 13732		17510000 -	17400001	P008209_174
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Collura, K. and Thompson, S. Direct Submission		17110000 17210000	17000001	1 1
REFERENCE 4 (bases 1 to 137327)  AUTHORS Wing, R.A., Yu, Y., Soderlund, C., Kim, HR., Rambo, T., Currie, J.,		16910000 17010000	16900001	P008209_168 P008209_169
Submitted (06-NOV-2) Arizona, 303 Forbes		16710000	16600001 16700001	
Currie, J., Collura, K. and Thomp Direct Submission		16510000 16610000	16400001 16500001	P008209_164 P008209_165
1 to 1373; Yu, Y., So		16310000 16410000	16200001	P008209_162 P008209_163
Submitted (09-OCT-20 Arizona, 303 Forbes		16110000 16210000	16000001	P008209_160 P008209_161
COllura, K. and Thompson, S. mission		15910000	15900001	P008209_158 P008209_159
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Rice Genomic Se Unpublished		15510000 15610000	15400001 15500001	
AUTHORS Wing,R.A., Yu,Y., Soderlund,C., Kim,HR., Rambo,T., Currie,J. and Collura,K.		15310000 15410000	15200001 15300001	P008209_152 P008209_153
Ehrhartoideae; Oryzeae; Oryza. REFERENCE 1 (bases 1 to 137327)		15110000 15210000	15000001	P008209_150
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		14910000	14800001 14900001	1 1
SOURCE Oryza sativa (Japonica cultivar-group) ORGANISM Oryza sativa (Japonica cultivar-group)		14710000 14810000	14600001 14700001	P008209_146 P008209_147
S Z		14510000 14610000	14400001 14500001	P008209_144 P008209_145
complete		14310000	14200001	P008209_142 P008209_143
DEFINITION Oryza sativa (japonica cultivar-group) chromosome 3 clone		14110000	14100001	P008209_140 P008209_141
206/c		13910000	13900001	P008209_138 P008209_139
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Query Match 34.4%; Best Local Similarity 85.7%; Matches 60; Conservative

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ESDEVKTVVAKAVSHLISVYGQQMQPILSALPPAHANALASFANRR"
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CCTCCATGCA 119430
                                                        CTTCCATGCA 133
                                                                                                                       CCTTGGCTATTCCGAACCAACAGAACACCTACTCCCAAACAATCACGCTGACTCATGCAA
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ASSSCFHASLFESKOHER VOHEL PEVTPKGCCTANLATDKONKSKESSQDVI DVDDECLL
ASSSCFHASLFESKOHER VOHEL PEVTPKGCCOTANLATDKYR PETAAQVCGNSKHVKF
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KSAAVFACAREQGRIVI ELMWPKTVVF PFLFHIKKLAQTLDLKEDKLHDSSHPSIKYI
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VETTKWPI I LI TSNKKDPPLPHLLAQL VLDFTY VPSAELLSHVDMI CKSEGVEI TVVPQ
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PCLYGHGI SNI VPBEVFFQQSSVPHLHEREVI SNQLCFPSESRAFEPASSFQNQLESNM
PGSI 5Q1 CCTFMSQG1 SCVPBLSF PMVGGTSASI SSDDLLSSLVSNGLSALRNESTYTA
SVVALEDTNKVENQMTDKPQKCMEDEVGETCEAYVELADRNDHASCSI TGYQLMDECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MGGSADPEAPTPTPSPSPSPAKATPSPASADGNRLRRCVQSKLS WGPPKAGGGGEAGAGLPLAAGDGTPEKVKKRGRPKKSEAGKFSSNRETTGLEQD SKDEVILVDESPQKKGRKGRGKNQGAALKVPNKHKKKLSLESTDGHESCQDLRSSQTQA VLPQKSPTSVDIDLVTGPSEASPVNDNVDALDNEDKPQLIVDLRSEANIAAEENRRLS SGKKMHPFFASRKIHKGAGQDILNVEDEDMDSLCAFERDPPLCPVHVLYELEVTMPIH
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FVADWEAHKAGRSSFSSASTRKPREEPPARDSPVRREVAAEEPPSLPAPAARPVLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAESVWLLSGKKNNDSCKVEHVQDTWNRLRQCHPVLPCDMNHNRSVSGALKRVSRVSD
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                                                                                                                                                                                                                                                                                                                                                                /gene="0J1041F02.6"
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BX950854
BX950854.12 GI:58190604
HTG.
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Lea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Vagnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Zea.
                                                           BX950854 171896 bp DNA linear Zebrafish DNA sequence from clone CH211-125M22, co
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nilarity 100.0%;
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llarity 100.0%;
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6 from Patent WO0160997.
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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/mol_type="unassigned
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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from Patent W00160997.
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Pred. No.
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Pred. No.
                                                                               171896 bp
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                                                              complete sequence
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                                                                                 VRT 03-FEB-2005
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                                                                                                     158544 AAGTAACATTCATCTAAAAATGCCTAAATATTTCATTTAAAATCTGAAATCTCAGTTTAA 158485
                                                                                                                                                                                            158604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSERO; Tr:, TREMBL; Mp:, WORNPEP; Information on the WORNPEP database can be found at the longer ac.uk/Projects/Celegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononuclectide A/T runs and conserved TA repeats. Where this is found the longest good mality representation will be
                                                              135 ACACGCACATATGTTTCCTGAA 156
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zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 25, 2005 this sequence version replaced gi:58368832.
                                                                                                                                                                                                                                                                              75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-FEB-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 171896)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: zfish-help@sanger.ac.uk
                   ACTCCCACATTTCTCATTTAAA 158463
                                                                                                                                        CTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATGCAA 134
                                                                                                                                                                                                                          TGGCATACTACATGCTTCATCCATCGTTCGTCCATCGTCCAAGCCTTGCCTATT 74
                                                                                                                                                                                            TGGGTTTGTCCATACTTGACCCAACGCTGGGTGTGTTAAAACAACCCAGCCTTTTAAAGT
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                                                                                                                                                                                                                                                                                                                                                                               /organism="Danio rerio"
/mol type="genomic DNA"
/db xref="taxon.7955"
/clone="CH211-125M22"
/clone_lib="CHORI-211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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is_from a CHORI-211 BAC library
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Pred. No. 3.1;
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AC104134
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1 (bases 1 to 110127)

1 (bases 1 to 110127)

Doebber,A., Haakenson,W. and Tomlinson,G.

Poebber, A., Hakenson, BAC clone RP11-525L16
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AC104134
                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (30-APR-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Direct Submission
Submitted (15-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
                                                                                                                                                                                                                       Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (04-DEC-2001) Genome
University School of Medicine,
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Submitted (20-MAR-2002)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                           SOURCE INFORMATION:
                                                                                                                                                                                                        http://genome.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://genome.wustl.edu
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                                                                                                    Frengen, E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The clone sequenced to the left is RP11-554H10, 2000 bp overlap; the clone sequenced to the right is RP11-450E9, 2000 bp overlap. Actual start of this clone is at base position 151996 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coworkers at http://www.chori.org
                         /translation="VFGNKMIIPSLDGALFQWDQDRESMETVPFTVESLLESSYKFGD
DVVLVGGKSLTTYGL6AYSGKWRYICSALGCKQWDDDRESMETQEEDILLLQRTQKTVRAIW
GPRSGABKMWRSVGHFELRYIPDMFTRAGFIESTFKPNENTTEESKIISDVESGGEAJM
DIVLBCSQLEKMPSVGHFELRYIPDMFTRAGFIESTFKPNENTTEESKIISDTSYTSN
DDVLBDEDITWSVAARGATENSVYLGWTRGQLVTQSSVRISKEFSSFKALESVNNENA
IIPLFTIKWFDLHSPSTRAFTPVLVGSDEFDKCLSUNDKFSHEEYSGMGALSILQPFVDMSV
IIPLFTIKWFDLHSGALTENTVLTGSDEFDKCLSUNDKFSHEEYSGMGALSILQPFVDMSV
IIPLFTKWFGTATTFLONPHYNKNIRKKDPVLLHWWKEIVATILFCIIATTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(67723..67923,68904..68966,72276..72377,
80861..81028,84653..8543,86541..86650,89505..89627,
93417..93529,98528..96048,97969..98091,98748..98888,
100430..100592,100805..101039,103259..103392,
105456...>105650))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(66728. 67923,68904. 68966,72276. 72377,
80861. 81028,8453. 85433,86541. 866590,89505. 89627,
93417. 93529,99528. 96048,97969. 98091,98748. 98888,
100430. 110592,100805. 101039,103259. 103392,
105456. 105650))
                                                                                                                                                                                                                                                                                                                             /note="Homo sapiens eukaryotic translation initiation
factor 2-alpha kinase 3 (EIF2AK3), mRNA.; H_NH0525L16.
This gene was based on gi(21361154)
Continued from H_NH0450E09.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="CpG_island (%GC=66.5, o/e=0.76, complement(66728. .105650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHIVKVPILNRWGPLMPFYQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAQLRDKEFYRPI PNPNPKLTDGYPA FKRPHMTAKDLGLPGFFPSQEHEATREDERKF
TSTCHFTYPASHDLHLAQGDPNQVLQSADFPCLVDPKHQPAAEMAKGYLLLPGCPCLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="CpG_island (%GC=62.5, 59905. .60161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="magykypgqdpydldiyqssshwydyqpyrkykysrytpqeqakl
daqlrdkefyrpipnpnpkltdgypafkrphmtakdlglpgffpsqeheatrederkf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This gene was based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="CpG_is
13008..13484
IVRRLFHPHPHRQRKESETQCQTENKYDSVSGEANDSSWNDIKNSGYISRYLTDFEPI
                                                                                                                                                                                                                       /protein_id="AAY24331.1"
/db_xref="GI:62988944"
                                                                                                                                                                                                                                                                          /product="unknown"
                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="EIF2AK3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="EIF2AK3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="EIF2AK3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAY24330.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Homo sapiens hypothetical protein
(FLJ25369), mRNA.; H_NH0525L16.1
|his gene was based on gi(22749356)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="FLJ25369"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oin (35632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="FLJ25369"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="FLJ25369"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="CpG_island (%GC=75.1, o/e=0.69,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oin (34638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="RP11-525L16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xref="GI:62988943"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type="genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .44562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 island (%GC=61.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .34769,35622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35658,36392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .36484,39039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .35658,36392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o/e=0.89,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o/e=0.83,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #CpGs=22) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #CpGs=24) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #CpGs=53)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #CpGs=20) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .36484,39039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .39571)
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87633 TGGGATTACAAGCGTGAGCCACTGTACCTGGCCAACCTATCTTTTTCTTCCTCCTCTCCA 87692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 ACTTCCATG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Faro, S., Felland, I., Grand-Pierre, N., Hacci, Gardyna, S., Gord, S., Graham, I., Grand-Pierre, N., Hacci, R., Gord, S., Gord, S., Graham, I., Grand-Pierre, N., Jones, C., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Leviner, R., Marota, P., Marchan, C., Macdonald, P., Major, J., Halbard, C., McCarthy, M., Meldrim, J., Meneus, L., Mibova, T., Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Mibova, T., Mathews, C., McCarthy, T., Neylar, J., Wengy, T., Naylar, J., O'Neil, D., Oliver, J., Mereson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Pierre, M., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Roy, A., R
                                                                                                                                                                                                                 Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70;
                                                                                      Boguslavkiy, L., Lucking Boguslavkiy, L., Cook, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iravers, M., Vassiller, Zainoun, J., Wyman, D., Young, G., Zainoun, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stojanovic, N., Talamas, J., Tesfaye Travers, M., Vassiliev, H., Viel, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rise, C., Rogov, P., Roman, J., Ko
Seaman, S., Severy, P., Smith, C.,
                                                                   Diaz,J.S., Dodge,
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-NOV-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Camarata,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 214946)
Birren, B., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     Research, 320 Charles Street, Cambridge, MA 02141,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cook, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC136896 214946 bp DNA linear PRI 21-MAR-2
Homo sapiens chromosome 15, clone RP11-86001, complete sequence.
            erreira, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC136896.6 GI:29135656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       omo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        irren, B., Nusbaum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCTCCAAG 87761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A., Cooke, P., Del
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bastien, V., Bloom, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKVDI FSLGLI LFELLYPFSTQMERVRTLTDVRNLKFPPLFTQKYPCEYVMVQDMLSP
SPMERPEAINI I ENAVFEDLDFPGKTVLRQRSRSLSSSGTKHSRQSNNSHSPLPSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTMDDVVKVGDFGLVTAMDQDEEEQTVLTPMPAYARHTGQVGTKLYMSPEQIHGNSYS
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JMQLCRKENLKDWNNGRCTIEERERSVCLHIFLQIAEAVEFLHSKGLMHRDLKPSNIF
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                                                                                                                                                                                                                                                                                                                                to 214946)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chang, J., Chazaro, B., Choepel, Y., Cully W., ke, P., DeArellano, K., Dewar, K., Diaz, J.S., ke, P., PitzGerald, M., Gage, D., Galagan, reira, P., FitzGerald, M., Gage, D., Galagan, M., Fetz, R., Wafez, R., W
FitzGerald, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.0%;
                                           Boukhgalter, B., Camarata, J., Chang, J., Cook, A., Cooke, P., Corum, B., DeArellano, K. ooke, S., Dooley, K., Dorris, L., Brickson, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34.6; DI
Pred. No. 3.6;
0; Mismatches
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me 15, clone RP11-86001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lander, E., Ali, A., Allen, N., Ander Bloom, T., Boguslavkiy, L., Boukhgalt Chazaro, B., Choepel, Y., Collymore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tesfaye, S., Theodore, J., Topham, K.,
Gage, D., Galagan, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zembek,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vo, A., Wilson, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson, B., Wu, X.,
Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Nicol,R., Norbu,C.,
willD., Oliver,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boukhgalter,B.,
      Gardyna, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRI 21-MAR-2003
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                                                                                                                                                                Choepel, Y.,
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                                                       Faro, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastten, V., Bloom, T., Boguslawky, L., Boukhgalter, B.; Camarata, J., Chang, J., Choepe Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, M., Tliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On MAr 21, 2003 this sequence version replaced gi:27877278. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, K., Macuean, V. Mandblad, P., Major, J., Manning, J., Mathews, C., Murphy, G. Macdonald, P., Meneus, L., Mihova, T., Mlenga, V., Murphy, G. Meneus, L., Mihova, T., Mlenga, V., Murphy, C., Ngyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 214946)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Mu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spencer, B., Stange-Thomann, N., Storal Talamas, J., Tesfaye, S., Theodore, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rachupka, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kamat, A., Karatas, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L27824
Center clone name: 860_0_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
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                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11 Human Male BAC" complement(1. .362) /rpt_family="HAL1" complement(823. .1431)
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complement (2941 . 3295)
/rpt_family="MER31B"</pre>
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note="single clone coverage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
mol_type="genomic DNA"
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Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MacLean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ., McCarthy, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choepel, Y.
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/rpt family="MIR"
complement (5336. .5464)
/rpt family "Family "Famil
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/rpt family="HAL1"
complement(25691. .25925)
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/rpt_family="MIR"
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/rpt family="MIR"
10252. .10587
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complement(8633..8
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complement(4758...499)
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/rpt_family="L3"
                                                                                                                                                                /rpt_fami
32586. .3
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/rpt_family="HAL1"
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26645.
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complement(26059..26582)
/rpt_family="MLT2B3"
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                                                       /rpt_family="L1M4"
33164. .33473
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complement(16057...1
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pt family="L1M1"
plament(19375. .20142)
t family="L1MB3"
15. .22910
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. .25023
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. .30036)
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ement(1000)
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                              family="AluY"
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Best Local S
Matches 68
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                                                                                                                                                                                            Assembly program: XGAP9; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 141058 bases at least Q40
Consensus quality: 141244 bases at least Q30
Consensus quality: 141289 bases at least Q20
Insert size: 141354; sum-of-contigs
Insert size: 152619; 10.9% error; agarose-fp
Quality coverage: 8.68x in Q20 bases; sum-of-contigs Quality
coverage: 8.12x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR847532.4 GI:57863691
HTG; HTGS PHASE1; HTGS ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pieces.
CR847532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-JAN-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquirtles: Catish-help@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk On Jan 15, 2005 this sequence version replaced gi:56309949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR847532 141554 bp DNI
Danio rerio clone DKEYP-86C9, WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Wellcome Trust Sanger Institute
* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: zKp86C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                ----- Summary Statistics
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complement(38001. ..
/rpt_family="L1MD1"
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/rpt_family="MLT1D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="MLT1D" 36941. .37015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="L1M4"
36696. .36751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .38449)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A linear HTG 15-JAN-2005
DRAFT SEQUENCE, 3 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8;
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Search completed: March 5, 2006, 21:55:32 Job time : 690.29 secs
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source
                                                                                                                                                                                                                                                                                                                                                        Query Match 21.5%; Score 33.8; DB 14; Length 141554; Best Local Similarity 52.5%; Pred. No. 6.6; Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps
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                                                                                      90342 TCAAAAAAAACTTATTAGTCC 90362
                                                                                                                                                                                90222 ACAGTGACCCCTACATCCTTGTGCCTCAATGCATATTGTACAAGTGTACAGAGGTTGGGT 90281
                                                                                                                             132 CAAACACGCACATATGTTTCC 152
                                                                                                                                                                                                         72 ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                                                                                                                                           12 ACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism "Danio rerio"
/mol_type="genmic DNA"
/db_xref="taxon:7955"
/clone="DKEYP-86C9"
/clone_1bEVP-86C9"
/clone_1b="DanioKeypilot"
1.10378
                                                                                                                                                                                                                                                                                                                                                                                                                                                            42428. .141554
/note="assembly_fragment:00621.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment:00017"
10479...42327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_fragment:00290"
12428. 141554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10378: contig of 10378 bp in length
10478: gap of 100 bp
42327: contig of 31849 bp in length
42427: gap of 100 bp
41554: contig of 99127 bp in length.
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0.1 2352 8 ACA48402 Aca48402 0.0 15734 6 ABN80329 Abn80329 19.5 64415 3 AAF22279 AA6222717 Ada22717 9.5 79467 10 ADB72455 Ade25965 9.5 79467 10 ADB72455 Ade595965 9.5 79467 10 ADB72456 Ade5965 9.5 79467 10 ADB72456 Ade5965 9.5 79467 10 ADB72456 Ade5965 9.5 Ade51436 Adb61436 Adb6143	93.0 158 5 AAH76334 Aah76334 34.4 2000 11 ACL38730 Acl38730 31.8 50 5 AAH76336 Aah76336 25.5 40 5 AAH76337 Aah76337 20.6 3267 12 ADK52131 Adk52131	ហហសសុហ	h Length DB ID Description	* SUMMARIES	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.	13: geneseqn2004bs:* 14: geneseqn2005s:*	 	4: geneseqn2001bs:* 5: geneseqn2001bs:*	ຊ	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	seq length: 0 seq length: 2000000000	of hits satisfying chosen parameters: 9993994	4996997 seqs, 3332346308 residues	table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	US-10-713-381-1_COPY_1155_1311 score: 157 : 1 cgtgtcatctcacatggcatcgcacatatgtttcctgaac 157	March 5, 2006, 17:08:23; Search time 104.48 Seconds (without alignments) 10014.946 Million cell updates/sec	nucleic search, using sw model	GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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המדבספים יומווימיי ליבס	****	٠.		,		i
Aafls843 Human	×	u	1478	18.1	28.4	5
Adb92108 Human	10 ADB92108	_	164702	18.2	28.6	4.
Adb96917 Human	10 ADB96917	ш	164702	18.2	28.6	Ü
Adb87934 Human	.0 ADB87934	L	164702	18.2	28.6	Ö
	ADB20845	8	164702	18.2	28.6	Ξ
Acf62730 Cancer	ACF62730	œ	164702	18.2	28.6	Ö
Continuation (6	.3 ABD32806_5	_	110000	18.2	28.6	9
Acn45162 Human gen	.1 ACN45162	_	51615	18.2	28.6	8
Adx13304 Plant	.3 ADX13304	_	3231	18.2	28.6	7
Adx11599 Plant	.3 ADX11599	_	2160	18.2	28.6	6
Abn67847 Streptoco	ABN67847	ق	1860	18.2	28.6	ഗ
Adw26566 Glycine	.3 ADW26566	_	1522	18.2	28.6	4.
Add71973 Human uri	10 ADD71973	_	1043	18.2	28.6	Ü
Aas32893 Human gen	AAS32893	4	778	18.2	28.6	N
Aas32892 Human gen	AAS32892	4	778	18.2	28.6	_
Ads57339 Bacterial	.3 ADS57339	_		18.2	28.6	0
Ada68284 Arabidops	ADA68284	8	1500	18.3	28.8	ø
Continuation (7 of	AAT42063	N	110000	18.6	29.2	œ
Aal62902 Vernonia	AAL62902	9	1475	18.6	29.2	27
Continuation (3 of	AAF22303_2	ω	110000	18.7	29.4	ð
Adf00796 Bacterial	.0 ADF00796	_	1185	18.9	29.6	ū
Aah13328 Human cDN	AAH13328	4	373	19.0	29.8	4.
Add33404 Mouse	10 ADD33404	ᆫ	396	19.1	30	w
Add33403 Mouse	10 ADD33403	_	378	19.1	30	22
Aah76335 Z. mays	AAH76335	ر.	30	19.1	30	21
Continuation (8	ADB12064_07	9	110000	19.2	30.2	0
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## ALIGNMENTS

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RESULT 2
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Best Local Similarity
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Best Local
                                                                                                           The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring ferrility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolls and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ms45; male; tissue-preferred; plant tissue; differentiated;
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Pred. No. 1.4e-42;
                                     Score 157; DB 2;
Pred. No. 2.4e-42;
; Mismatches 0;
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maize; hybrid seed; fertility;
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Best Local Similarity
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tive 0; Mismatches 0;
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CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC

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Kendall

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RESULT 5
AAH76333
ID AAH7
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AC AAH7
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AC AAH7
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AT 29-0
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Best Local S
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                  29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an MS45 male tissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                               AAH76333 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 46; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-514772/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z. mays Ms45 male tissue-preferred regulatory region encoding
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                                                                                                                                                                                                                                 CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
                                                                                                                                                                                                                                                                        AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                                                                                                                                                                                                                                                                                                     CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC
                                                                                                                                                                                                                                                                                                                                                                                   CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC
                                                                                                                                                                                            CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
                  (first entry)
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                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 157; DB 5;
Pred. No. 2.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1394;
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Best Local
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             WO200160997-A2
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    mays Ms45 male tissue-preferred regulatory region fragment

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                                                                                                                                                                                                                                                                     AAH76334 standard; DNA; 158
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                                                    Zea mays.
                                                                                           hybrid seed; ds.
                                                                                                          Ms45; male tissue; regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 47; 50pp; English.
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    mays Ms45 male tissue-preferred regulatory region encoding

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157; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTGTCATCTCACATGCCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTTCCATCGTCC
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                        (first entry)
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Pred. No. 2:4e-42;
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Length 1394;

Indels

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RESULT 7
ACL38730
ID ACL38730
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AC ACL3
AC ACL3
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AC ACL3
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AC ACL3
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COLS
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BS;
XW
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Best Local Simi
Matches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription of the MS45 gene. A method of mediatring male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -38 to -195 bases upstream of the DATA box of a Z. mays MS45 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for
   22-JUN 2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-035277P.
21-NOV-2001; 2001US-0332132P.
                                                                                                                                                                                                                                                                                                                           Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 158 BP; 41 A; 50 C;
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                                                                                                                                                                                                                                                                 WO2003008540-A2
                                                                                                                                                                                                                                                                                                                                                                                  ss; abiotic stress agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rice stress-regulated promoter SEQ ID NO:17293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACL38730;
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                                                                                                                                                 21-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
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                                                                                                                                                 2002WO-US019668
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                                                                                                                                                                                                                                                                                                                                                                                                             tolerance; transgenic plant; plant; cereal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 146; DB 5;
Pred. No. 6.1e-39;
0; Mismatches 0
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The invention relates to novel abiotic stress responsive polynucleotides cand polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the cress, osmotic stress or any of their combinations. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                              New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                Claim 48;
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SYGN ) SYNGENTA PARTICIPATIONS AG
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                                                                                                                                                                                                                                                                                                              SEQ ID NO 17293; 89pp; English.
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T, Provart
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N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glazebrook J,
D, Zhu T;
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밁 Ś 밁 S Query Match Best Local S Matches 60 1879 1819 124 64 60; Similarity CCTTGGCTATTCCGAACCAACAGAACACCTACTCCCAAACAATCACGCTGACTCATGCAA CTTCCATGCA 133 CCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA CCTCCATGCA 1888 Conservative 34.4%; Score 54; DB Pred. No. 1.2e 0; Mismatches <u>.</u> 1.2e-07; ches 10; DB 11; Length 2000; Indels 0 Gaps 123 1878 0

Sequence 2000 BP; 616 A; 370 C; 355 G;

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RESULT 8
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    mays Ms45 male tissue-preferred regulatory region fragment

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                                                                                                                                               Albertsen MC,
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Query Match
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Matches 50
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The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription of the M845 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment upstream of the TATA box of a Z. mays M845 male-tissue preferred regulatory region nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
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hybrid seed; ds.
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8.1e-07;
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2774 TTCTTTTTCTCACCTCCCCCCCGATTTCTTTGTACCTCACTTTCATTTTGGCCTTTAAGTT 2833

27 TECTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAG

Query Match Best Local S: Matches 66

Similarity

20.6%;

Score 32.4; DE pred. No. 2.5; 0; Mismatches

DΒ

Length 3267; Indels

Conservative

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Sequence 3267 BP; 1029 A; 658

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RESULT 10
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Matches
                               The invention relates to detecting atopic dermatitis or psoriasis comprising assaying the levels of expression of an indicator gene at a rash site and non-rash site of a person with atopic dermatitis or psoriasis, comparing these levels with those of a healthy person, and determining that if the levels of indicators are higher or lower then this indicates the disease. Also included are a reagent for detecting atopic dermatitis or psoriasis, a kit for screening for treatments, a transgenic non human vertebrate animal models for the diseases, an agent for inducing the diseases in mice and a DNA chip for assaying for the indicator genes. The method is used for treatment, detection and animal models for research of atopic dermatitis and psoriasis. The present sequence is a Mouse atopic-dermatitis/psoriasis-associated EST
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                                                                                                                                                                                                                                 Detecting atopic dermatitis or psoriasis of expression of an indicator gene at a rash person with atopic dermatitis or psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; ss; EST; atopic dermatitis; anti-inflammatory; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse atopic-dermatitis/psoriasis-associated
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14-MAY-2003; 2003JP-00136544.
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                                                                                                                                                                                                          Claim 20; SEQ ID NO 164; 484pp; Japanese.
                                                                                                                                                                                                                                                                                     WPI; 2004-214514/20.
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                        (expressed sequence tag).
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40; Conser
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i K;
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Pred. No.
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C; 590 G; 990 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rash; expressed sequence tag.
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ACA48402/c
                            the 613 antisence sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid concoling a polypeptide whose expression is inhibited by the antisense converged or its fragment whose expression is inhibited by the polypeptide or its fragment whose expression is inhibited by the carried containing the vector; (3) an isolated containing the vector; (3) an isolated converged conv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang
Wall
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; SEQ ID NO 36272; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200277183-A2
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                 proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                candidate molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELITRA PHARM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zamudio C,
Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148
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                 of an organism. The
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antisense nucleic acids are useful for homologous nucleic acids requi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen
Forsyth
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2352 BP;
                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for cellular proliferation to isolate candidate molecules for radrug discovery programs, or for screening homologous nucleic aci required for proliferation in cells other than S. aureus, S. typ K. pneumoniae or P. aeruginosa. The present sequence is one of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2001; 2001WO-EP007536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation; antidiabetic; cytostatic; anticonvulsant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human chemically modified disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCCTGACTGTGCCCAAAGCCAAAGGAAGCATACTCCTGAAAAATCTGTGCTACATCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.2;
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of genes associated with development successful for AFDI and comprising one of 350 specification such as ACCPN, ADPN, or AFDI and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with development genes, in particular disease related to homeobox containing development genes, in particular disease related diseases, syndromes

The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II of genes associated with development selected from 87 genes listed in ACCDN ADFN, or AFD1 and comprising one of 350

(II)

Claim 1; SEQ ID NO 346; 27pp; English

development genes, in parti genes (HOX), like diabetes, associated with congenital

ce diabetes, cancer, apoptosis related congenital heart disease, epilepsy, di

diseases

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                                                                                                                                                                                                          Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15734 BP; 3630 A; 744 C; 4234 G; 7126 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF22279
                        The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors,
                                                                                                                                                                   Claim 102; Page 321-335; 1449pp; English.
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18-MAY-1999;
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7-SEP-1999;
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53; Conser
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antibodies,
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99US-0127409P.
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99US-0153584P.
99US-0154603P.
99US-0172493P.
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Pred. No. 9;
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Sequence 64415

BP; 18698

A, 13554

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18980

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Sequence

79467 BP;

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RESULT 14
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ID ADA02
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CC recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CC A nucleic acid, a polypeptide (especially an antibody) that specifically CC binds to the protein, and a biochip comprising CA nucleic acid or C fragments thereof. The sequences of the invention were identified using CC oncogenic retroviruses, which insert into the genome of the host organism CC at random. Many of these do not carry transduced host oncogens or gathogenic trans-acting viral genes, meaning that cancer incidence is a CC direct consequence of the effects of proviral integration into host consequence of the effects of proviral integration into host carcinoma (especially breast cancer, prostate cancer, lymphoma or CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC darkent consequence of the effects of proviral integration in particular consequence of the propagation of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The CC present sequence expresents a specifically claimed murine CA nucleic acid consequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained CC from the control of the printed specification, but was obtained CC from the control of the printed specification.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to recombinant carcinoma associated (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant nucleic acid encoding carcinoma associated useful for preparing compositions for treating carcinomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse Nfatc1 carcinoma associated gene, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2003
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                                         ftp.wipo.int/pub/published_pct
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                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences from mouse and human (ADA01482-ADA03094) wbinant_carcinoma associated proteins (CAP) encodec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1235; 245pp; English.
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RESULT 15
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                                                                                                         Query Match
Best Local Similarity
Matches 57; Conserv
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Best Local Similarity 56.4%;
Matches 57; Conservative
                                                                                                                                                                                                The invention relates to a novel recombinant nucleic acid comprising a nuclectide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-2001; 2001US-00798586.
23-OCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
                                                                                                                                                                   Sequence 79467 BP; 18256 A; 19684 C; 20062 G; 20204 T; 0 U; 1261 Other;
                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 283; 2304pp; English.
                                                                                                                                                                                                                                                                                                                                                               New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-239337/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse Nfatc1 gene
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                                          53839 CACACACACACACACACACACACACACACAGCTTGTGGCTC 53879
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                                                                          TCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCAT 110
                                                                                                         Conservative
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                                                                                                      19.5%; Score 30.6; D
56.4%; Pred. No. 28;
tive 0; Mismatches
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53839 CACACACACACACACACACACACACAAGCTTGTGGCTC 53879

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Search completed: March Job time: 107.48 secs

DB 9;

Length 79467;

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est6:*
7: gb_est6:*
8: gb_est7:*
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Gapop 10.0 , Gapext 1.0
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157
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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CC256933 CGMDQ20TM
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CM324514 104 819 1
CM44575 fsbboolf1
CE588104 tigr-gss-
CO689495 bc11-25n6
AG366773 Mus muscu
CZ727957 OC Ba005
BB505306 BB505306
CM871470 She2h63-4
CL026582 CH216-23G
C1026582 CH214-23G
A1744861 tr16b06.x
C2446438 UGI XGG22
CW558661 OA ABA013
CW597425 OA ABA013
CX424281 UGI XZG4
CR575123 CR575123
CW599444 OA ABA013
CX40428 UGI XZT35
DN096073 UGI CABE6
A1064657 Drosophil
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CZ954687	DU054394	BH752563	AK028832	BC048853	AL322183	BF682258	AL05540	BI453933	BB004373	BE134144	BX517541	BF020472	BE133867	AA673664	BX528623	CN243061	BE448824	BF225639	BE632212	AW990724	AJ746802	BE690384	
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# ALIGNMENTS.

Qy	Query Match Best Local Matches 15	FEATURES SOURCE		AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM ORGANISM	RESULT 1 CC656939/c LOCUS DEFINITION
1 CGTGTCATCTCACATGCCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC 60	Query Match 100.0%; Score 157; DB 9; Length 687; Best Local Similarity 100.0%; Pred. No. 2.2e-39; Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Seq primer: TF Class: methylation filtered. Location/Qualifiers 1. 687 1. 687 //organism="Zea mays" //mol_type="genomic DNA" /strain="B73" //b_xref="taxon:4577" /clone="ZMMBMa0554D15" /clone=lib="ZM 0.7 1.5 KB" /note="Vector: DBCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"	TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org	Whitelaw.C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Buddiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002) Other_GSSs: OGMDQ20TM Contact: Cathy Whitelaw	CC656939.1 GI:32060231 CC656939.1 GI:32060231 GSS. Zea mays Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 687)	CC656939 687 bp DNA linear GSS 19-JUN-2003 OGWDQ20TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0554D15, genomic survey sequence.

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DEFINITION
                  RESULT 3
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 CC656933 963 bp DNA linear GSS 19-JUN-2003 OGWDQ20TM ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0554D15,
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1 (bases 1 to 915)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 301-838-5843
Fax: 301-838-0208
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Other_GSSs: OG1AG08TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cathy Whitelaw
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/note="Vector: pBCSK-; Site_1: HincII;
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CW324514
CW324514.1
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Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                     GSS.
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Class: methylat
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    Martienssen, R.A.
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ilarity 100.0%;
Conservative 0,
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/strain="B73"
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752 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC
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Nhite-law, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Renick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Unpublished (2002)
Other GSS8: OGMDQ20TV
1 (bases 1 to 702)

Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                   CW324514 702 bp DNA linear GSS 31-OCT-2004 104 819_11477203_148_35910_078 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11477203, genomic survey
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Sorghum.
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/clone lib="ZM 0.7 1.5 KB"
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Pred. No. 2.4e-39;
Mismatches 0;
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                                                                                                                                                                                                              Sorghum bicolor (sorghum)
Sorghum bicolor (sorghum)
Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Eukaryota, Viridiplantae, Ililopsida, Poales, Poaceae, PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
Clade; Panicoideae; Andropogoneae; Sorghum.
1 (Dases I to 296)
1 (Dases I to 296)
1 (Dases I to 296)
1 (Pilck, E., Rohlfing, T., Fries, J., Bradford, K., Momenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.F., McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CW445575
fsbb001f170m16k0 Sorghum
Sorghum bicolor genomic c
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Seq primer: SWfor Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Bedell JA
                                       Orion Genomics, LLC
4041 Forest Park Ave,
Tel: 314 615 6979
Fax: 314 615 5975
                                                                                                                                                                                                                                                                                                                                                                                                                                                CW445575.1
                                                                                                Contact: Bedell JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCCATGCAA 134
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11 Forest Park Ave,
1314 615 6979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s: methylation filtered
quality sequence stop: 702:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hum genome sequencing by Biol. 3 (1), e13 (2005)
                                                                                                                                                      num genome sequencing by methylation filtration Biol. 3 (1), e13 (2005)
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jbedell@oriongenomics.com
fsbb001f170 row: m column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bedell@oriongenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: leaf; Vector; pBGSK(-); Site 1: HincI; DNA prepared from purified nuclei was randomly—sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Sorghum bicolor"

mol_type="genomic DNA"

cultivar="ATx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:55193536
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93.0%;
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                                                                             St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 bp DNA linear GSS 02-NO methylation filtered library (LibID clone fsbb001f170m16, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methylation filtration
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                                                                                  MO 63108, USA
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KEYWORDS
SOURCE
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AUTHORS
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CE588104/c
LOCUS
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    Query Match
                                                                                                                                                                                                          source
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Class: methylation filtered
High quality sequence stop:
High cocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Laurasiath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tigr-gss-dog-17000366359543 genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                             The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)

    (bases 1 to 636)
    Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and

                                                                                                                                                                                                                                                                                                                           Contact: Kirkness BP
The Institute for Genomic Research
Department of Eukaryotic Genomics,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                       Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CE588104.1 GI:36904885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                             /organism="Canis familiaris"
/mol type="genomic DNA"
/strain="standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/clone_lib="Dog Library"
/note="Site 1: BetXI; Librarie
peripheral Dlood"
                                                                                                                                                                                                                                                                     ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 9 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
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/mol_type="genomic DNA"
/cultivar="ATx623"
                                                                                                                                                                                                                               ocation/Qualifiers
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lone="fsbb001f170m16"
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       24.1%;
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Pred. No. 0.00042;
0; Mismatches 10
         Score 37.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ćraniata; Vertebrata; Euteleostomi;
heria; Carnivora; Fissipedia; Canidae;
                                                                                       Libraries
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9712 Medical

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SOURCE
ORGANISM
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CO689495/c
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                                                                        KEYWORDS
                                                                                            VERSION
                                                                                                                                                DEFINITION
                                                                                                                                                                                 RESULT 8
AG366773/c
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                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 58.4 Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                      ORGANISM
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                                                                                        sequence.
AG366773
AG366773.1
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                                                                                                                                                                                                                                                                                                                                                                                                  66,
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DG11-25n6 DG11-kidney Canis familiaris cDNA 3', mRNA sequence.
CO689495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schlueter,T., Hermanns,J., Weindel,M.,
Henrich,J. and Loebbert,R.
Dog arrayTAG cDNA clone collection
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                 Mus musculus molossinus (Japanese wild mouse)
                                                                                                                                              AG366773
Mus musculus molossinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Thomas Schlueter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 643)
Schlueter, T., Herma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CO689495.1 GI:50638161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTTTTTCCCAGTTCAAGGCATCCTTGTTTGGACCCAAGGGTATACCTCATTTTTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
/clone_lib="DG11-kidney"
/note="Organ: kidney; Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9615"
/tissue_type="kidney"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain="Beagle"
                                                                                            GI:47977978
                                                                                                                                                                                                                                                                                                                                                                                                                 24.1%;
58.4%;
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DNA,
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clone:MSMg01-170B12.TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vector: Dog pBluescript LION"
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7;
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AUTHORS
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CZ727957
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Best Local Similarity
Matches 69; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              659 ACATNAATAACNCCCCCCNANNAAACCANNANAACCCCGCAATTTTTTNANAANNATAAA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-2 Suechiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Teukuba Institute of Physical and Chemetr, The Institute of Physical Adams of Physic
Oryza coarctata (Porteresia coarctata)
Oryza coarctata
Oryza coarctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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R.Site
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                                                                                                                                                            GSS.
                                                                                                                                                                                                                     OC_Ba0055L24.f OC_Ba Oryza 5', genomic survey sequence. CZ727957
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Direct Submission
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Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y.,
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/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xret="taxon:57486"
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Moriwaki, K.
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                                                              1 (bases 1 to 700)
Arakawa, T., Carninci, P., Pukuda, S., Furuno, M., Kawai, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramafsu, M. and Hayashizaki, Y., RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Unpublished (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB505306 TOO bp mBB505306 RIKEN full-length enriched, female mammary-gland Mus musculus ct
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi, Muroidea; Muridae; Murinae; Mus.
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Mammalia; Eutheria;
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Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
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Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., S
           Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                    BB505306.2 GI:16442791
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University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036,
                                                                                                                                                                                                                                                                                                                                                                             fus musculus (house mouse)
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BACKWARD: CAC TCA TTA GGC ACC CCA
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/lab_host="DH10B"
/clone_lib="OC__Ba"
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/db_xref="taxon:77588"
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78.6%;
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Pred. No. 2.7;
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ed, 10 days lactation, adult
cDNA clone D730002G06, mRNA
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GATACCTACTCCCAAACCAATCCATCTTACTCATGCAACTTCCATGCAAACAACACCACATAT 146
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Local Similarity hes 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               further details.
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Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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TTCTTTTTCTCCCCTCCCTCTGATTTCTTTGTACCTCACTTTCATTTTGGCCTTTAAGTT 254
                                                   TGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAG
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                                                                                                                                                                                                                                                                                                                                                    was cleaved with BamHI and XhoI. Vector: a modifivelence
                                                                                                                                                                                                                                                                                                             Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
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Project of Genome Exploration Research Group in R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adult female mammary gland"
/note="Site 1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
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/mol_type="mRNA"
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M., Yoneda,Y., Ishikawa,T., Ozawa,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="mammary gland"
dev_stage="10 days lactation, adult"
lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 one="D730002G06"
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                                                                                                                                   21.7%;
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                                                                                                      ; Score 34; DB 2; Pred. No. 8.3; 0; Mismatches
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u,N., Sugahara,Y., Shibata,K.,
                                                                                                                                                                DB 2; Length 700;
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Kiyosawa,H., Yamanaka,I
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K., Tanaka,T.,
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CW871670/c
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                                                                                                                                                                                             121 CAACT 125
                                                                                                                                                                                                                        178 GAACTACACCACCACAGÁCACCACAGÁCACATACACCCÁCACACACATTTAACACAGA 119
                                                                                                                                                                                                                                                                            238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CW871670 734 bp DNA linear GSS 12-FEB-2005 she2h63-44.g 013.abl Whole-genome shotgun library of the elephant shark (aka elephant fish) Callorhinchus milii genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular Genetics Lab
Institute of Molecular and Co
61 Biopolis Drive, Singapore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Callorhinchus milii (elephantfish)
Callorhinchus milii
                                                                 CL026582 1677 bp DNA CH216-23G24_Sp6.1 CH216 Xenopus tropicalis CH216-23G24, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A compact cartilaginous fish model genome Curr. Biol. 15 (3), R82-R83 (2005)
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CW871670
Xenopus tropicalis
Xenopus tropicalis
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Fax: 65 6779 1117
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Venkatesh, B., Tay, A., Dandona, N., Patil, J.G.
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68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mcbbv@imcb.a-star.edu.sg
genome shotgun sequences (
                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="Testis" /clone \overline{1}ib= "Whole-genome shotgun library of the elephant shark (aka elephant fish)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Callorhinchus milii"
/mol_type="genomic DNA"
/db_xref="taxon:7868"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="Male"
                                          GI:40470443
                                                                                                                                                                                                                                                                                                                                            21.5%;
               (western clawed frog)
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Pred. No. 9.8;
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christoph
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 GCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCA
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Kremitzki,C., Carter,J., McPherson,J., Warren,W.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: (
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
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Washington University School of Medicine
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tr16b06.x1 NCI_CGAP_Ov23
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Xenopodinae; Xenopue; Silurana.
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                                                                                                                                                                                 Hominidae; Homo.
1 (bases 1 to 440)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                      Homo sapiens
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
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cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell line="Stock 248 F7A2, /clone_lib="CH216" /note="Vector: pTARBAC2.1; CBAC library"
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/mol_type="genomic DNA"
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/db_xref="taxon:8364"
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                                                                                Christopher Moskaluk, M.D.,
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IMAGE:2218451 3',
    Sequencing
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/db_xref="taxon:4532"
/clone="0A_ABAGO80BO7"
/tissue_type="young leaves"
/lab_host="DH10B T1 phage resistant"
/clone lib="0A_ABa"
/clone lib="0A_ABa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

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Scoring table:
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Listing first 45 summaries
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Perfect score:
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Match Length DB
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-513-999C-8379 US-08-946-026-9	US-09-949-016-12928 US-09-949-016-12740	US-09-593-828-11	US-09-949-016-15039	US-09-949-016-13038	US-09-949-016-13037	US-09-949-016-12088	US-09-134-001C-678	US-09-949-016-17130	US-09-949-016-11989	US-09-596-002-39	US-09-949-016-17576	US-09-949-016-13779	US-09-949-016-14091	US-09-949-016-17368	US-09-949-016-12703	US-08-184-012C-5	US-07-882-925A-5
Sequence 8379, Ap Sequence 9, Appli	Sequence 12928, A Sequence 12740, A	Sequence 11, Appl		Sequence 13038, A	Sequence 13037, A	Sequence 12088, A	Sequence 678, App	Sequence 17130, A	Sequence 11989, A	Sequence 39, Appl	Sequence 17576, A	Sequence 13779, A	Sequence 14091, A	Sequence 17368, A	Sequence 12703, A	Sequence 5, Appli	Sequence 5, Appli

ALIGNMENTS

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ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
STREET: Box 1000
CITY: Johnston
STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: PIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweeney. Patricia A.
                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                    SEQUENCE CHARACTERISTICS
LENGTH: 1394 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                         STRANDEDNESS:
                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                          NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,733 REFERENCE/DOCKET NUMBER: 0578
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6037523
                                                             nucleic acid
  TYPE:
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DNA (genomic)
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100.0%; Score 157; DB 3; Length 1394;

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Patent No. 6037523
                                                                                                                                          Matches
                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
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COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
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NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
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APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/880,499 FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: 800
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                                                                                                                                                                                                                            DNA (genomic)
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16073
LENGTH: 385136
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                                                                                                                                 US-09-543-681A-1081
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1081, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                             SEQ ID NO 1081
LENGTH: 1185
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Best Local :
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                                            Matches
                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(385136)
                                                                                                                                                   ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: n = A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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o. 6812339
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  35 CAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTA 94
                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                            Conservative
                                                              18.9%;
59.5%;
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                                          <u>,</u>
                                          Score 29.6; DE Pred. No. 3.4; 0; Mismatches
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Pred. No. 14;
0; Mismatches 41; Indels 0;
                                                                                  DB 3;
                                            34;
                                                                                    Length 1185;
                                              Indels
                                            0
                                          Gaps
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940 CAACAATTTGTTTTTTGTCCACCAGAAAGACCTAACCCATTTTCTCCCCAAGGACATATCTA 881

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RESULT 6
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STEANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
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Best Local Similarity 51.5
Matches 67; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      677275 ACTTRANATTCAGCCTGCTTGCTTGCTCTATTGCATTTGCATTAAATGCAAGCATAGCCT 677216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/476,102

RILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                     132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: 3 1/2 inch disket COMPUTER: Dell Pentium OPERATING SYSTEM: MS DOS v6.22 SOFTMARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCCAAACAATCCATCTTACTCA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/557,884 FILING DATE: 25-Apr-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                CAAACACGCA 141
                                                                                                                                                                                           ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09557884
                                                                                                              CAACCAACCA 677146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Rockville
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                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                     63;
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TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-643-990A-1
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US-10-158-865-1/c
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GENERAL INFORMATION:
APPLICANT: Robert D.
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fragm |
Patent No. 6846651
                                                                                 Sequence 1, Application US/10158865
Patent No. 6846651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.6
Best Local Similarity 51.5
Matches 67; Conservative
                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3 1/2 inch diskette

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/643,990A

ETITAG DATA: 23-ANG-2000
                                                                                                                                                                                                                                                                                                                    677275 ACTITABATTCAGCCTGCTTGCTTGCTATTGCATTTGCATTABATGCAAGCATAGCCT 677216
                                                                                                                                                                                                                              677155 CAACCAACCA 677146
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FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                        132 CAAACACGCA 141
                                                                                                                                                                                                                                                                                                                                                                 72 ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 ACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCT 71
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STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23-Aug-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1830121 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hamilton O. Smith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.6%; Score 29.2; DB 3; Length 1 51.5%; Pred. No. 63; ative 0; Mismatches 63; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 1830121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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SOFTWARE: PatentIn version 3.1 SEQ ID NO 1 FILE INVENTION: Thereof, and Uses Thereof FILE REFERENCE: PB186P2C1D1 CURRENT APPLICATION NUMBER: US/10/158,865 CURRENT FILING DATE: 2002-06-03 PRIOR APPLICATION: PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR FILING DATE: 1995-06-07
PRIOR PELICATION NUMBER: US 08/426,787
PRIOR PELICATION DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1 FEATURE:
NAME/KEY: misc\_feature
LOCATION: (47036). (47036)
OTHER INFORMATION: n equals a,t,c, TYPE: DNA
ORGANISM: Haemophilus influenzae
FEATURE:
NAME/KEY: misc feature
LOCATION: (4747)..(4747) NAME/KEY: misc feature LOCATION: (45732)..(45732) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (44975)...(44975) NAME/KEY: misc\_feature LOCATION: (44905)...(44905) OTHER\_INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (44416)..(44416) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (40808)..(40810) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (36636)..(36636) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (36551)..(36 NAME/KEY: misc feature LOCATION: (36543)...(36543) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (29298)..(29298) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (10150)..(10150) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (9921)..(9921) LOCATION: (4747) .. (4747)
OTHER INFORMATION: n equals OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (45593)..(45593) OTHER INFORMATION: n equals OTHER INFORMATION: n OTHER INFORMATION: n equals ENGTH: 1830121 .. (36551) equals a,t, a,t, a,t, a,t, a,t, a,t, a,t,c, a,t, a a,t,c, a,t,c, a,t,c, a,t,c, 'n ò ò ò Ģ ò ò Ö or g 9 8 or or or õ ဝူ õ ç õ or P õ ω ω g φ ω ω ø ω ω ω g ω ω

NAME/KEY: misc feature LOCATION: (121344)..(121344) OTHER INFORMATION: n equals : FEATURE: FEATURE:
NAME/KEY: FEATURE: FEATURE: NAME/KEY: misc feature (107248)...(107248) FEATURE: NAME/KEY: misc\_feature LOCATION: (65309)..(65309) OTHER INFORMATION: n equals FEATURE: FEATURE: NAME/KEY: FEATURE: NAME/KEY: NAME/KEY: misc feature LOCATION: (122167)...(122167) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (120038)...(120038) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (119924)...(119924) OTHER INFORMATION: n equals FEATURE: NAME/KEY: misc\_feature LOCATION: (119750)..(119750) OTHER\_INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (117136)..(117136) OTHER INFORMATION: n equals FEATURE: NAME/KEY: misc\_feature LOCATION: (105121)...(105121) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (102696)..(102696) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (100091)..(100091) OTHER\_INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (65313)...(65313) OTHER INFORMATION: n equal NAME/KEY: misc feature LOCATION: (55369)..(55369) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (51805)..(51805) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (51786)..(51786) NAME/KEY: misc\_feature LOCATION: (51334)..(51334) OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (80024)..(80024) OTHER INFORMATION: n equals OTHER INFORMATION: n equals OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (51602)..(51602) equals a,t a,t, a,t, a,t, a,t, a,t, a,t, a,t,c, a,t,c, a,t,c, a,t,c, a,t,c, a,t,c, a,t,c, a,t,c, ò 'n ò ò ò ò 'n ò ò ò ç ဝူ ဝူ õ õ õ õ 얹 o r õ ç õ õ ç ç õ õ õ ω ω ıo g ιΩ ú ω ω ω Ø ω ω g ø g ω ω ιΩ

misc\_feature

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RESULT 8
US-09-049-016-14712/c
US-09-049-016-14712/, Application US/09949016
; Sequence 14712, Application US/09949016
Patent NO. 6812239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
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Best Local 9
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a,t,c, or g
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LOCATION: (147197)...(147197)
OTHER_INFORMATION: n equals
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LOCATION: (140398)..(140398)
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COCATION: (139910) ... (139910)
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LOCATION: (131360)...(131360)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,c,
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals
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LOCATION: (145171)..(145171)
DTHER INFORMATION: n equals
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OCATION: (142750)..(142750)
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                                                                                                                                                                                                                                      677275 ACTITAAATTCAGCCTGCTTGCTTGCTCTATTGCATTTGCATTAAATGCAAGCATAGCCT 677216
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ION: (145058)..(145058)
INFORMATION: n equals a,t,c,
                                                                                                                                                                                       132 CAAACACGCA 141
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                                                                                                                                                                                                                                                                                                                                           12 ACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCT
                                                                                                                                                                                                                                                                                                                                                                           ch 18.6%;
1 Similarity 51.5%;
67; Conservative
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Pred. No. 6
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                IN KNOWN GENES
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              ASSOCIATED
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; ORGANISM: Human
US-09-949-016-14712
RESULT 10
US-09-949-016-15502
; Sequence 15502, Application US/09949016
; Patent No. 6812339
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US-09-949-016-14713/c
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; ORGANISM: Human
US-09-949-016-14713
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Best Local S
Matches 45
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 14712
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version SEQ ID NO 14713
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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                                                                                                                                                                        355 TCATCCAATAGTTTCCACTACTAATCCATGATGGAACTGAGTACTAATCAAGCCAATATT 296
                                                                                                         295 CTCATGTAACAT 284
                                                                                                                                          115 CTCATGCAACTT 126
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                                                                                                                                                                                                           55 TCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTA 114
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Pred. No. 27;
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US-09-949-016-15502
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US-09-949-016-17447
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SEQ ID NO 17447
LENGTH: 41815
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Best Local S
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Patent No. 6812339
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APPLICANT: VENTICH: J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-09-08
NUMBER OF SEQ ID NOS: 207012
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-031,498
PRIOR FILING DATE: 2000-9-08
PRIOR FILING DATE: 2000-9-08
PRIOR FILING DATE: 2000-9-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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33118 ATGTCACATAGAGACATGCATGTA 33141
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                                          122 AACTTCCATGCAAACACGCACATA 145
                                                                                                                                  62 AGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 TGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATT
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                                                                                          AGACATGCAGATTCACACACATCCGCATAGCTGCTCCTACGGATCCCTGGTCACTCATTC
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nilarity 63.2%;
Conservative
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                                                                                                                                                                                                    17.8%;
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Pred. No. 27;
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); Mismatches
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RESULT 12

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Sequence 14149, Application US/09949016

| Sequence 14149, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION: GENES ASSOCIATED TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-10-20
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR FILING DATE: 2000-10-20
| PRIOR APPLICATION NUMBER: 60/237,768
| PRIOR FILING DATE: 2000-10-03
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR PILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 14149
| LENGTH: 11490
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US-09-949-016-191201
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION UNMERE: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 191201
LENGTH: 601
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Best Local
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                      ORGANISM: Human
                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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nes 47; Conserv
5582
                                                                                          5642 CAGGGCCTCTGCCTTGCCCTCCCCCTGCCCCACCTCACCAGGAGGAAGCCCACGC 5583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 CATGCAACTTCCATGCAAACA 137
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                                           98 CCAAACAATCCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 GTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACT 116
                                                                                                                                     38 CCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTC 97
                                                                                                                                                                                    62;
CCTTGCACACCTGATGCCACATCCGCTTGAGTGGCAGGCGAGTGAAGATGTTGCCCCAAA 5524
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58.0%;
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Pred. No. 11
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US-09-949-016-16740
                                                                     ; OTHER INFORMATION: Description of Artificial Sequence; No. 6846621e = ; OTHER INFORMATION: synthetic construct US-09-937-8628-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16740
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/S-09-937-862B-37
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Query Match
Best Local Similarity 55.1
Matches 54; Conservative
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                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US00/07828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL001307
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                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPLICANT: VENTER, J. Craig et al.
TILE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                             JRRENT APPLICATION NUMBER: US/09/937,862B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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No. 6846621
                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 GGTTTTÁCACACACACACA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 CCATGCAAACACGCACATA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 TGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 TGTCAACCGTGATCCAACAGTATAATTAGTTCTTAGGAATTCCTCTCTCACAGGTAACTA 129
                                                                                                                                                                                                                                                           PLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                INVENTION: TYPING OF HUMAN ENTEROVIRUSES
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                                                                                                                                                                                                           FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09937862B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for Windows Version 4.0
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                     17.6%;
55.1%;
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                                                                                                                                                                                                                                                           60/127,464
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     0; Mismatches
                     Score 27.6;
Pred. No. 15;
                                      DB 3; Length 927;
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       44;
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       Gaps
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53 CATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCT 112

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. Gourch Completed. March 5 2006 22.36.21	611 CTTTTGTGGGCATTACAAACGCGTACTCACATTTTTAT 648	113 TACTCATGCAACTTCCATGCAAACACGCACATATGTTT 150	551 CATCATCAAACCCCTCAATATTCTACACCTATGGAACAGCACCACCACACATTTCGATCC 610	

Search completed: March 5, 2006, 22:36:21 Job time : 48.8947 secs

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# GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

Title:
Perfect score:
Sequence: Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 OM nucleic - nucleic search, using sw model Total number of hits satisfying chosen parameters: Searched: Run on: US-10-713-381-1\_COPY\_1155\_1311 157 March 5, 2006, 23:29:31; Search time 225.751 Seconds (without alignments) 5750.985 Million cell updates/sec 9793542 seqs, 4134689005 residues 1 cgtgtcatctcacatggcat.....cgcacatatgtttcctgaac 157 19587084 The state of the s

Database : Published Applications NA\_Main:\*

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9: /cgn2 6/ptodata/1/pubpna/US10L\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US11L\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is, derived by analysis of the total score distribution.

### SUMMARIES

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19.0	19.1	19.1	19.1	19.2	19.2	19.2	19.4	19.5	19.5	19.5	19.6	19.6	20.0	20.1	20.5	25.5	31.8	93.0	100.0	100.0	100.0	Query Match
617	843	843	30	1754382	1266	436	52001	79467	559	559	1122	601	565	2352	399	40	50	158	1394	1394	255	Query Match Length
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Sequence 10490, A Sequence 285326,	Sequence 170626,	Sequence 170626,	Sequence 4, Appli	Sequence 6651, Ap	Sequence 2923, Ap	Sequence 153052,	Sequence 11, Appl	Seguence 223, App	Sequence 244811,	Seguence 244811,	Sequence 1496, Ap	Sequence 778732,	Sequence 871704,	Sequence 36272, A	Sequence 9081, Ap	Sequence 6, Appli	Sequence 5, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 9, Appli	Description

RESULT 2 US-10-711-381-1 ; Sequence 1, Application US/10713381 ; Publication No. US20040221331A1

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	28.8	28.8	28.8	29	29	29	29	29	29	29.2	29.2	29.2	29.2	29.6	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	
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	Sequence 21722, A	Sequence 21721, A	Sequence 805392,	Sequence 85365, A	Sequence 222445,	Sequence 222444,	Sequence 222445,	Sequence 222444,	Sequence 78606, A	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 11, Appl	Sequence 2154, Ap	Sequence 179264,	Sequence 179264,	Sequence 254612,	Sequence 254612,	Sequence 12385, A	Sequence 57018, A	Sequence 285328,	Sequence 285327,	

## ALIGNMENTS

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•						Query Match Best Local Matches 15	10-713-381	TYPE: DNA	LENGTH:	SEQ ID NO	SOFTWARE:	NIMBER OF	PRIOR	CURRENT	CURRENT			APPLICANT	APPLICANT:	APPLICANT:	APPLICANT:	ADDITONT	IDI1C	Sequence	RESULT 1 US-10-713-
	121	75	61 .	15	1	atch cal			TH: 255	S			APPLICATION NUMBER: 08,			NI 40		ANT:	ANT:	ANT:		ċ	Publication No.	, 9	381-
Ξ	CAACT	AAGCC	AAGCC	CGIGI	CGIGI	₽.	2	702 m	Ü			SEO TO	CATIO	ING D	LICAT	INVENTION:	INVENTION:	KENDALL,	HUFFMAN,	GARNAAT,	FOX.	ALBERTSEN	NO.	Appli	ω .
	TCCAT	TIGCC	TIGCC	CATCT	CATCI	100 larity 100 Conservative	may 5	200			In Ve	ID NOS: 24	N NUMI	ATE:	ION NO			ALL, 3		AAT,	FOX, TIMOTHY W	TO RU	520040	cation	
TOWARD	GCAAAC	FATTCI	PATTCI	CACATO	CACATO	100.0%; 100.0%; htive					r. 2.0	24	3ER: 0	FILING DATE: 2003-11-14	APPLICATION NUMBER:	OSING	MALE TISSUE-	TIMMY L.	GARY	CARL W.		MARC	US20040221331A1	Application US/10713381	
	ACGCA	GAACC	GAACC	GCATA	GCATA	0,0%;					_	2.3	18/880	11-14		SAME	SSUE-	٢			•	J	141	07133	
CATAT	CAACTTCCATGCAAACACGCACATATGT	TCTGAACCAAGAGGATACCTACTCCCAAAC	AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG	CGTGTCATCTCACATGGCATACTACATGC	CGTGTCATCTCACATGGCATACTACATGCTTGT	Score Pred. Mis							, 499		US/10/713,381		PREFERRED							81	
	GITTC	GATAC	GATAC	-1-	IGCTT	ore 157; ed. No. 2. Mismatches							,	•	381									٠	
TTCCTGAAC	FTCCTGAAC	CTACT	CTACT	TGTTCAACCGTTCGTC	⊢]	DВ 1е-											REGULA								
771	2 157	CCAA	CCCAAJ	ACCGT	CAACCGTTCGT	۲				,							ATORY								
		CAATCC	CAATC	CGICI	CGICI	Length Indels						٠					REGULATORY REGION AND								
		ATC	CATCI	TTGTTCCATCGTCC	TGTTC	255;											N AND								
		TTACTO	TACTO	CATCG	GTTCCATCGTCC	0; Ga											METHOD								
		TCATG 1				Gaps											AO GO								
		134	120	74	60	0																			

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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 2
LENGTH: 1394
TYPE: DNA
ORGANISM: Zea may8
US-10-713-381-2
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US-10-713-381-2
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SEQ ID NO 1
LENGTH: 1394
TYPE: DNA
ORGANISM: Zea mays
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APPLICANT: ALBERTSEN, MARC
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL
                                                                                                                                                 Matches
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Publication No. US20040221331A1
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CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
TILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
                                                                                                                                                 Local Similarity
les 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 157; Conserv
                                                                1215 AAGCCTTGCCTATTCTGAACCAAGAGATACCTACTCCCAAACAATCCATCTTACTCATG
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CGTGTCATCTCACATGGCATACTACATGCTTCTTCAACCGTTCGTCTTGTTCCATCGTCC
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                                                                                                                                             100.0%; Score 157; DB 8; llarity 100.0%; Pred. No. 3.8e-43; Conservative 0; Mismatches 0;
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; ORGANISM: Zea mays
US-10-713-381-3
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) ORGANISM: Zea mays
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                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 50
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10713381
Publication No. US20040221331A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 157; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                                   FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
                                                                                                                                                                                                                                              APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNART, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUB-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                           PRIOR APPLICATION NUMBER: 08/880,499 PRIOR FILING DATE: 1997-06-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ALBERTSEN, MARC C.
                                                                                                                          NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1215 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG 1274
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HUFFMAN, GARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOX, TIMOTHY W.
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Pred. No. 1e-39;
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Query Match Best Local Matches 5

50;

Conservative

Similarity

DB 8; 5.7e-07

Length 50;

0;

75 CTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 124

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ublication No. US20040227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
VUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/713,381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                            RIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0-674-124A-9081/c
OTHER INFORMATION: chr5.fa.07frz.139538206
                                                                                                                                                                                                                                                                                                                                                     TLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
TLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
TLE REFERENCE: ORIN-003CIP
                                                                                            ID NO 9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
                                  GANISM: Homo sapiens
                                                                                                                                                                                                         APPLICATION NUMBER: JP2000-112699 FILING DATE: 2000-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                9081, Application US/10674124A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 124
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40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Ver. 2.0
                                                                                                             SEQ ID NOS: 27110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                 CATION NUMBER: JP2002-383869
                                                                                                                                                                                    CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BERTSEN, MARC C.
                                                                                                                                                                                                                                                                                                                                    ON NUMBER: US/10/674,124A
                                                                                                                                                                                                                                                                                                                                                                                                                                Hidetoshi
                                                                                                                                                                                                                                            2000-10-30
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Pred. No. 0.0014;
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US-10-282-122A-36272/c
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OTHER INFORMATION: Located on chromosome 5
ORGANISM: Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.5%;
Local Similarity 61.2%;
es 52; Conservative
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tion No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 ATTTTGAAGAAAACAGTGGGCCACCCTCAAAAAACCCCAAACTACTCATCTAACTTAAAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 AAAAAACCACACATTTGTGATGAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 САЛАСАСССАСАТАТСТТТССТСАЛ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 ATTCTGAACCAAGAGGATACCTACTČCCAAACATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wall, Daniel
Trawick, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                   ON NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Distance between 3'-terminus of neighbour sequence of sequence listing upward to telomere on chrosomal short arm and 5'-terminus of this base sequence : 250186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence : 128437212
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                                                                                                                                                      2001-02-
                                                                                                                                                                                                                                                                                                                                                                                      2000-05-23
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                                                                                                                                                                                                     MBER: 60/257,931
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                                                                                                  ion data removed - See File Wrapper or PALM
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                                                                                                                                                                    60/267,636
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                                                                                                                                                                                                                                                                    60/242,578
                                                                                                                                                                                                                                                                                                                                    60/230,335
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                                                                                                                                   60/269,308
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0; Mismatches
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Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
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FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 871704
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US-09-925-065A-871704
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                                                                                                                                                                                                                                                                                                                       RESULT 10
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US-09-925-065A-871704
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                                                                                                                                                                                                                          Sequence 778732, Application US/09925065A Publication No. US20050228172A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                      334 TCATGATAATTTTGAACAARGAG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 AACTTCCATGCAAACACGCACATATGTTTCCTGA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 ATCCTGACTGTGCCCAAAGCCAAAGGAAGCATACTCCTGAAAAAATCTGTGCTACATCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                       64 CCTTGCCTATTCTGAACCAAGAG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GICATCICACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCTCTTGCTTGGAAGAGCCCATGCTTGGTTTAACGCCCTTCTGTCTCCGTCTTGAAAT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTTCAGCAAAAGAACGTTCAATTTTTTCCTGA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31.4; DI
Pred. No. 3.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 565;
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PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 778732
LENGTH: 601
TYPE: DNA
ORGANISM: Homo Bapiens
US-09-925-065A-778732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1496, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                            SEQ ID NO 1496
LENGTH: 1122
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Best Local (
                                                                                                                                      Matches
                                                                                                                                                     Best Local
                                                                                                                                                                         Query Match
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 CAAACACGCA 141
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                                120 GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
                                                                    234 AÁCÁCTGACÁ 225
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                                                                                                  60 CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT 119
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                                                                                                                                     Similarity 56; Conserv
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Zhou, Yihua
Cao, Yongwei
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TCAGATCCACAAATCGCACCCTCCCATATCTGCTGAAC 216
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Barbazuk, Brad
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Pred. No. 7;
0; Mismatches
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Pred. No. 5.5;
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                                                                                                                                                                       DB 7; Length 1122;
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RESULT 12 US-10-027-632-244811 · Sequence 244811, Application US/10027632

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RESULT 13
US-10-027-632-244811
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; ORGANISM: Human
US-10-027-632-244811
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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SEQ ID NO 244811
LENGTH: 559
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                                                                                                                                                                                                                          PRIOR PELICATION NUMBER: US 60/218,006
PRIOR PELICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                          PLICANT: Wang, David G.
TLE OF INVENTION: Identification and Mapping of Single Nucleotide
TLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE: 108827.129
                                                                                                                                     APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
                                                                                                                                                                                              APPLICATION NUMBER: US 60/193,483 FILING DATE: 2000-03-29
APPLICATION NUMBER: US 60/146,002 FILING DATE: 1999-08-09
                                                                                                                    APPLICATION NUMBER: US 60/167,363
                                                                    APPLICATION NUMBER: US 60/156,358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 GAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATGCAAACACGCACA 143
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; ORGANISM: Human US-10-027-632-244811
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SEQ ID NO 244911
LENGTH: 559
TYPE: DNA
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Best Local Similarity
Matches 69; Conserv
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CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 09/747,377
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IITLE OF INVENTION: NOVEL COMPOSITIONS AND
FILE REFERENCE: A-71087/RMS/DCF
                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (10089)..(10620)
OTHER INFORMATION: "n" at positions 10089 to 10620
                                                                                                                                       NAME/KEY: misc feature
LOCATION: (20762)..(20781)
OTHER INFORMATION: "n" at positions 20762 to 20781 can be
                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (5502)..(5521)
OTHER INFORMATION: "n" a
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LOCATION: (4099)..(4369)
OTHER INFORMATION: "n" a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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LOCATION: (5502)..(552
                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (13273)..(13370)
DTHER INFORMATION: "n" at
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                     NAME/KEY: misc_feature
LOCATION: (46579)..(46
                                                                        OCATION: (30751)..(30916)
OTHER INFORMATION: "n" at
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ION: (46579)..(46772)
INFORMATION: "n" at positoins
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o. US20040072264A1
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, NAME/KEY: misc feature
; LOCATION: (77382)..(77401)
; OTHER INFORMATION: "n" at positions 77372 to 77401 can be any base US-10-052-482-223
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US-10-317-273-11
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Publication No. US20040110158A1

GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie
APPLICANT: Tamara Balac Sipes
TITLE OF INVENTION: MODULATION OF MITOCHONDRIAL RIBOSOMAL PROTEIN L13 EXPRESSION
FILE REFERENCE: RTS-0478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 19.5%; Score 30.6; D
Best Local Similarity 56.4%; Pred. No. 39;
Matches 57; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/317,273
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 159
SEQ ID NO 11
                                                                                                                                                                                          Query Match 19.4%;
Best Local Similarity 61.2%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 11220
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

LOCATION: 11187, 11188, 11189, 11190, 11191, 11192, 11193, 11194, 11195,

LOCATION: 11196, 11197, 11198, 11199, 11200, 11201, 11202, 11203,

LOCATION: 11204, 11205, 11206, 11207, 11208, 11209, 11210, 11211,

LOCATION: 11212, 11213, 11214, 11215, 11216, 11217, 11218, 11219

OTHER INFORMATION: n = A,T,C or G

FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature

LOCATION: 11154, 11155, 11156, 11157, 11158, 11159, 11160, 11161,

LOCATION: 11163, 11164, 11165, 11166, 11167, 11168, 11169, 11170,

LOCATION: 11171, 11172, 11173, 11174, 11175, 11176, 11177, 11178,

LOCATION: 11179, 11180, 11181, 11182, 11183, 11184, 11185, 11186,

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

LOCATION: 11121, 11122, 11123, 11124, 11125, 11126, 11127,

LOCATION: 11130, 11131, 11132, 11133, 11134, 11135, 11136,

LOCATION: 11138, 11139, 11140, 11141, 11142, 11143, 11144,

LOCATION: 11146, 11147, 11148, 11149, 11150, 11151, 11152,

OTHER INFORMATION: n = A,T,C or G

FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53839 CACACACACACACACACACACACACACAAGCTTGTGGCTC 53879
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                      110 TCTTACTCATGCAACTTCCA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 CTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTC 151
                                                                                                                                50 TTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGGATACCTACTCCCAAACAATCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 TCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCAT 110
TCTTTCTCAGCAAACTTCTA 20134
                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                 Score 30.4; 1
Pred. No. 39;
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11137,
11145,
11153
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Search completed: March 6, 2006, 03:55:07 Job time: 227.751 secs

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
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Gapop 10.0 , Gapext 1.0
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157
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Match Length DB ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7218535 seqs, 1096242582 residues
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/ Cgn2_6/ptcdata/2/pubpna/PcT_NEW_PUB.seq: *
/ Cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq: *
/ Cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq: *
/ Cgn2_6/ptcdata/2/pubpna/US10_NEW_PUB.seq: *
/ Cgn2_6/ptcdata/2/pubpna/US11_NEW_PUB.seq: *
/ Cgn2_6/ptcdata/2/pubpna/US10_NEW_PUB.seq: *
/ Cgn2_6/ptcdata/2/pubpna/US10_NEW_PUB.seq: *
US-09-925-065A-153052
US-09-925-065A-283327
US-09-925-065A-283327
US-09-925-065A-283328
US-09-925-065A-13385
US-09-925-065A-13385
US-10-750-65A-80339
US-10-750-623-47517
US-11-750-623-47517
US-10-750-623-47517
US-09-925-065A-33976
US-09-925-065A-33976
US-09-925-065A-33976
US-09-925-065A-33976
US-09-925-065A-33976
US-09-925-065A-33976
US-09-925-065A-33980
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US-09-925-065A-33980
US-09-925-065A-33980
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US-09-925-065A-778732
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                                                                                                                                                                                                                     Sequence 185, Appl
Sequence 13, Appl
Sequence 153052,
Sequence 285326,
Sequence 285327,
Sequence 285328,
Sequence 12385, A
Sequence 1295, Appl
Sequence 805392,
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Sequence 778732,
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Matches 50
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27.4	27.6		27.8	27.8	27.8	27.8	27.8	27.8	~1	27.8	28	28	28	28	28	28	28	28	28	28	28	28	28	
17.5	17.6	17.6	17.7	17.7	17.7	17.7	17.7	17.7	17.7	17.7	17.8	17.8		17.8			•	•	17.8		17.8	17.8	17.8	
531	1724	1724	393323	3242	3242	1476	1476	576	560	541	2750	2750	2341	2341	2327	2327	2327	2327	1740	1740	1691	1691	801	
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-09-925-065A-9591	US-10-750-623-55178	-10-750	-773-23	US-10-750-623-58624	US-10-750-185-58624	US-10-750-623-37809	US-10-750-185-37809	US-09-925-065A-757513	US-09-925-065A-945788	US-09-925-065A-427091	US-10-750-623-39884	US-10-750-185-39884	US-10-750-623-30272	US-10-750-185-30272	US-09-925-065A-686354	US-09-925-065A-686353	US-09-925-065A-686352	US-09-925-065A-686351	US-09-925-065A-553736	US-09-925-065A-553735	US-09-925-065A-33979	US-09-925-065A-33978	US-09-925-065A-32051	
Sequence	Segnence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	ø	Sequence	Sequence		æ	Sequence	
	68127, A	2 6	App	24	58624, A	•	•	757513,	945788,	427091,		•	30272, A	٠	4	686353,	686352,	686351,	553736,	553735,		ά.	32051, A	

ALIGNMENTS

# RESULT 1 US-09-925-065A-871704 ; Sequence 871704, Application US/09925065A ; Sequence 871704, Application US/09925065A ; Publication No. US20040181048A1 ; GENERAL INFORMATION: APPLICANT: Mang, David G. TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REFERENCE: 108027.135 CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT APPLICATION NUMBER: US 60/243,096 PRIOR PRILING DATE: 2000-10-24 PRIOR FILING DATE: 2000-10-24 PRIOR PILING DATE: 2000-11-30 PRIOR APPLICATION NUMBER: US 60/250,992 PRIOR APPLICATION NUMBER: US 60/250,992 PRIOR APPLICATION NUMBER: US 60/250,992 PRIOR PILING DATE: 2001-01-36 PRIOR APPLICATION NUMBER: US 60/250,992 PRIOR PILING DATE: 2001-01-36 PRIOR APPLICATION NUMBER: US 60/250,992 PRIOR PILING DATE: 2001-05-09 PRIOR PILING DATE: 2001-05-09 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD ID NOS: 957086 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD ID NOS: 957086 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD ID NOS: 957086 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD ID NOS: 957086 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD ID NOS: 957086 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD ID NOS: 957086 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD ID NOS: 957086 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD ID NOS: 957086 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD ID NOS: 957086 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD ID NOS: 957086 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD ID NOS: 957086 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD ID NOS: 957086 PRIOR PILING DATE: 2001-05-09 NUMBER OF SQD NOS: 957086 PRIOR PILING DATE: 2001-05-09 PRIOR PILING

US-09-925-065A-778732/c

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US-11-117-187-185; Sequence 185, Application No.
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                                                US-11-117-187-185
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR PPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 778732, Application US/09925065A Publication No. US20040181048A1
  Query Match
                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 778732
LENGTH: 601
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NUMBER OF SEQ ID NOS: 212
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: ARCD:309US
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                                                                                                                                           TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                   OTHER INFORMATION: N =
                                                                                     NAME/KEY: modified base LOCATION: (9960)..(2114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                        FEATURE:
                                                                                                                                                                                                     ENGTH: 64415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68;
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o. US20050266560A1
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ilarity 52.3%;
Conservative
    19.5%;
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Pred. No. 4.3;
0; Mismatches
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  Score 30.6;
                                                                     or T/U
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  DB 12;
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Length 64415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 153052, Application US Publication No. US20040181048A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/11121086 Publication No. US20050266459A1 GENERAL INFORMATION:
                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 153052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
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APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR PILING DATE: 2004-05-04
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                     NUMBER OF SEQ ID NOS: 957086
                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                         PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 108827.135
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ORGANISM: Homo sapiens
                     TYPE: DNA
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ORGANISM: Homo sapiens
                                           ENGTH:
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                                                                                                                                             APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                  FILING DATE: 2001-01-16
                                                                                                                                                                                      APPLICATION NUMBER: US 60/261,766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 CTCATGCAACTTCCATGCAAACACGCACATATGTTT 150
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US-09-925-065A-153052
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; Sequence 285326, Application US/09925065A
; Publication No. US20040181048A1
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US-09-925-065A-285326
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                                                                                                                                                                                                                                                                                 -09-925-065A-285327
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PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION UNMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/925,065A
                                                                                                  FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                             PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                    equence 285327, Application US/09925065A
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                                                                                                                                                       TLE OF INVENTION: Identification and Mapping of Single TLB OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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FILING DATE: 2000-11-20
APPLICATION NUMBER: US 60/250,092
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l Similarity 60.5%;
49; Conservative
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                LICATION NUMBER: US 60/252,147
ING DATE: 2000-11-20
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60.2%; Pred. No. 6.1;
tive 0; Mismatches
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Pred. No. 9;
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US-09-925-065A-285327
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US-09-925-065A-285328
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US-09-925-065A-12385
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LENGTH: 617
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Best Local
       Sequence 12385, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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49; Conserv
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PRIOR FILING DATE: 2000-11-30 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2001-01-16
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PRIOR APPLICATION NUMBER: US 60/289,846
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PRIOR APPLICATION NUMBER: US 60/250,092
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433 TACCTGCACTGAAGTTAAATG 453
                                       134 AACACGCACATATGTTTCCTG 154
                                                                             373 TGTGTAGAAATTTAATACATACTTCCAAACAATCCAGAGTTTTGTAGCAACTTATACTCC 432
                                                                                                                    74 TCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATGCA 133
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milarity 60.5%;
Conservative 0
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US20040181048A1
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Pred. No. 9;
                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                   Score 29.8;
Pred. No. 9
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US-11-117-187-209/c
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12385
LENGTH. 1.22
                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 209
LENGTH: 611587
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                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Arabidopsis thaliana
-11-117-187-209
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
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APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 212
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                                          270144 TCTCTCCTGCCAAGCGAATGGATTTGTCATGCATTTGTTGCTAACTGCCGACACAAGCTG 270085
                                                                                                                                                  Local
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Similarity 50.3%;
                                                                                                                                                18.7%;
Similarity 52.0%;
GCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTC 127
                                                                                   TCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTT 67
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Pred. No. 11;
0; Mismatches
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                                                                                                                              0; Mismatches
                                                                                                                                                Score 29.4;
Pred. No. 91;
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human G
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-01-20
PRIOR PILING DATE: 2000-01-06-06
PRIOR PILING DATE: 2001-01-16
                                              ; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-47517
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US-09-925-065A-805392
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US-09-925-065A-805392
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SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 805392
LENGTH: 544
                                                                                                                    SOFTWARE: PatentIN version 3.1
SEQ ID NO 47517
LENGTH: 1370
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Best Local
Query Match
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                      APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FARTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING
FILE REFERENCE: MMII100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-05-09
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KERR, Richard
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18.3%; Score 28.8;
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Pred. No. 18;
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Length 1370;
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RESULT 14
US-09-925-065A-845392
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; ORGANISM: Bovine 19866880570548
US-10-750-623-47517
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SEQ ID NO 47517
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Best Local
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                                                                                                           PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
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TITLE OF INVENTION, METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/925,065A
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                                                                                                                                                                                                                                                                                                  PILCANT: Wang, David G.
TLE OF INVENTION: Identification and Mapping of Single
TLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
LE REFERENCE: 108827.135
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on No. US20050287531A1
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57; Conservative
                                                                                       PLICATION NUMBER: US 60/261,766
SEQ ID NOS: 957086
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ROSENFELD, David
HOLM, Tom
BATEC
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DATE: 2002-12-31
                                    TE: 2001-01-16
ON NUMBER: US 60/289,846
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Pred. No. 2
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US-09-925-065A-33976/c
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US-09-925-065A-845392
                                                                                                                                                                                                          Search completed: March 6, 2006, 10:32:44
Job time: 164.89 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT: Wang, David 's Identification and Mapping of Single ITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome ILE REFERENCE: 108827...35
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Scoring table:

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Query Match Length

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BD062176 BD062177 IJ Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

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JOURNAL
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Best Local Similarity
Matches 1311; Conserv
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Patent: JP 2001520523-A 2 30-OCT-2001;
PIONEER HI ERED INTERNATIONAL INC
PN JP 2001520523-A/2
PD 30-OCT-2001
PP 30-OCT-2001
PP 30-UN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMAN,
PI CIZN15/82, CIZN15/29, CIZN9/24, CIZN9/22, CIZN9/10, CIZN9/00 PC
C C CTOPOlogy: Linear;
CC Topology: Linear;
CC To
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JP 2001520523-A/2.
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1 (bases 1 to 1394)

Albertsen, M.C., Fox, T.W., Garnaat, C.W.,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini
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                                                                                                                                                                                                                                                                                                                                  CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
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                            CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCCATCAAGGGCCCTTTCGGATGGCCCA
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CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Db 601 TTATATCGAÂAGGTĀĀGCTĀTGĀCGTTCAĞĀTTTTTCTTTTTCATTCTTGTTATTTTTTT Qy 661 ATTGTTTTATATACATTTTCTTCTTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA			1261 CCATCTTACTCCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
Db 541 CÁAGCATÁTTTTCGAAAGAGÁCAAATTATGTTACAGTTTACAAACATCTAAGAGGGACAAA  Qy 601 TTATATCGAAAGGTAAGCTATGAGATTTTTCTTTTTCATTTCTTTGTTATTTTTTTT			1201 TIGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260 1261 CCATCTTACTCATGCCATGCCAAACCACACACACTTTCCTGAAC 1311
Db 481 CGAAAGCTATCATGTAAATGTTTAAAGAAACATCTATTAAAAACACCACGATCCTCTTAAAAAAA  Oy 541 CAAGCATATTCGAAAGAAGAAAATTATGTTACAGTTTACAACATCTAAGAGGGACAAA  Oy 541 CAAGCATATTCGAAAGAGACAAATTATGTTACAGTTTACAACATCTAAGAGGGACAAA			
Qy 421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAATAACCAAGATAACTAATCCACT	-		1081 TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA 1140
Qy 361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG Db 361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG		1	1021 TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAGAGAAATCAGTTTTAAGTCATTGTCCC 1080
Qy 301 TTATTATTCTTTAGATATTTATTTAGTTTTTGGAAAATAACAAACTTATACTTTTGGTA	<u>-</u>		961 GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020 
Qy 241 CGACACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA 300 Db 241 CGACACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA 300	-		901 TGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTG 960
OY 181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA			841 TTCAAAAAAATTAGTTTATTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT 900 
Qy 121 CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCCGATGTTCCCAT			781 TITCTGATTITTTAAGAGCTAGTITGGCAACCCTGTTTCTTCAAAGAATITTGATTIT 840
OY 61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAACTTCCACGGGTGCATGAT Db 61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT Db 61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT	,		721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC 780 
Oy 1 CCATGGTGTCTCTATGAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC			661 ATTGTTTTATATACATTTTCTTCTCTTTACAATAGAGTGATTTTČTTCCGATTTTATAAA 720 
Query Match 100.0%; Score 1311; DB 6; Length 1394; Best Local Similarity 100.0%; Pred. No. 7.2e-228; Matches 1311; Conservative 0; Mismatches 0; Indels 0;			601 TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT 660
"unassigned DNA" taxon:4577"			541 CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAA 600 
PIONEER HI-BRED INTERNATIONAL, INC. (US) FEATURES Location/Qualifiers source 1. 1394 forganism="Zea mays"			481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA 540
REFERENCE 1 AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T. TITLE Male tissue-preferred regulatory region and method of using same JOURNAL Patent: WO 0160997-A 1 23-AUG-2001;			421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATATAACCAAAGTAACTAATCCACT 480
NISM			361 GGGCCTCAGCATGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG 420
AX224394 AX224394 1394 bp DNA linear LOCUS DEFINITION Sequence 1 from Patent W00160997. ACCESSION AX224394 VERSION AX224394 GI:15554636 KEYWORDS Zea may9		, s , s , s , s , s	CGAGACGTATCGGGTGGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATACTTTTTGTGTATATTTTTTTT
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y Match Local Similarity 100.0%; Score 1311; Local Similarity 100.0%; Pred. No. 7 hes 1311; Conservative 0; Mismatcher 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAA;	source 11394 /organism="Zea mays" /mol_type="unassigned DNA" /db_xref="taxon:4577" ORIGIN	Male tissue- Patent: WO 0 PIONEER HI-E	clad 1 Albe		ITION Sequence 2 from Patent W0016097. SION AX224395 ON AX224395.1 GI:15554637		OY 1261 CCATCTTACTCATGCAACTTCCATGCAACACGCACATATGTTTCCTGAAC	OY 1201 TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT	OY 1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGT	OY 1081 TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA	Qy 1021 TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAGAAGAAATCAGTTTTAAGTCATTGTCCC	Qy 961 GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT	OY 901 TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTAGTTTG	Oy 841 TICAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT	Qy 781 TITCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTC	Qy 721 ATGACTATAAAGTCATTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAAT	Db 661 ATTGTTTTTATATACATTTTCTTCTTTACAATAGAGTGATTTTCTTCCGATTTTATAAA
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Qy 1021 TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAAAATCAGTTTTAAGTCATTGTCCC 1080	Qy 961 GCCAGCCCCATAAATTATTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020 	Qy 901 TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTG 960	OY 841 TTCAAAAAAATAGTTTATTTTCTCTTTATAAATAGAAAACACTTAGAAAAATAGAGT 900 [	Qy 781 TTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTC	Qy         721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC 780	Qy 661 ATTGTTTTATATACATTTTCTTCTCTCTACAATAGAGTGATTTTCTTCCGATTTTATAAA 720	Qy 601 TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTT 660	Qy         541 CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAA 600	Qy 481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA 540	QY 421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAATAACCAAAGTAACTAATCCACT 480	Qy 361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG 420	QY 301 TTATTATTCTTTAGATATTATTTAATTTTTGGAAAAATAACAAACTTATACTTTTGTGTA 360	Qy 241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA 300	Qy 181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240	Qy 121 CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT 180	Qy 61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	

QY 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	Query Match 100.0%; Score 1311; DB 15; Length 3343; Best Local Similarity 100.0%; Pred. No. 6.2e-228; Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RIMRYMLEGPRAGEVEVFANLPGFPDNVRSNGRGOFWVAIDCCRTPAGEVFAKRPMLR TLYFKFPLSLKVLTWKAARRMITVLALLDGEGRVVEVLEDRGHEVMKLVSEVREVGRK LWIGTVAHNHIATIPYPLED" ORIGIN	DYREVKHELA FYGENGSHEZHINGASELRRGZIEFVGEVEGES I EFDLQGRGFYAGLA DYREVKHELA FYGENGSFENDKASELRRGZIEFVGEVEGES I EFDLQGRGFYAGLA DGRVVRMGEELAGNETFAVNLPDMSEEVCANGVNSTTRKQHEKEEFCGRFLGIEFHGE TGELYVADAYYGLMVVGQSGGVASSVAREADGDFI RFANDLDVHRNGSVFFTDTSNRY SKKDHLMILLEGEGTGRILKYDPETGSVHYVLKGLVFPNGVGJSEBOLDGRIFT	/ COMMING PLATEST / product= "male fertility protein" / protein_id="AAK52489.1" / protein_id="AAK52489.1" / db_xref="GI:14028757" / t-z=n_lation_imprount_nepsprogramy.put_repsprount_fertility.put_	/product="male fertility protein" /product="male fertility protein" /product="male fertility protein" /oin(1392. 1768,18982182,22802447,25342942) /gene="M845" /code="M845"	gene <1392. >2942 /gene="Ms45" mRNA join(<1392. 1768,18982182,22802447,2534>2942) /gene="Ms45"	~~~	50131-1004, USA Location/Qualifiers 1.3343 "Tea mays"	AUTHORS FOX. THIMMEL! M.R. and Albertsen, M.C.  AUTHORS FOX. Timmel! M.R. and Albertsen, M.C.  TITLE Direct Submission M.R. 2001) Trait and Technology Development, Pioneer JOURNAL Submitted (13-MAR-2001) Trait and Technology Development, Pioneer JOURNAL Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston,	Fox, T.W., Tr Cloning of N Unpublished	Euk Spe cla	AF3	z	1261	Db 1201 TIGTTCCATCCTAAGCCTTGCCAATCTGAACCAGAGGATACCTACTCCCAAACAAT 1260  Qy 1261 CCATCTTACTCCATGCAACCTCCCATGCAAACACATATGTTTCCTGAAC 1311	Db 1141 GGTTCGGCAGCTCTCGGTGTCATCTCACATGGCATACATGCTTGTTCAACCGTTCGTC 1200  OY 1201 TTGTTCCATGGTCAAGCCTTGCCTATTGTGAACCAAGAGGATACCTACC	Db 1081 TGAGATGTGGGAACGATAGCCACGTAATCATAGGTGCTAAGGTGCTACGTCA 1140  Qy 1141 GGTTCGGCAGGTCTCGTGTGTCAACGATAGCATACATGCTTGTTCAACGGTTCGTC 1200
	1021 TTCTCTAG	961 GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAATCTGAGCTAT	Qy 901 TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTG 960	Qy 841 TICAAAAAAATTAGTITATITTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT 900	Oy 781 TITCTGATTITTTAAGAGCTAGTITGGCAACCCTGTTTCTTCAAAGAATTTTGATTTT 840	Db 721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGAAAAATC 780	661 ATTGTTTTTATATACATTTTCTTCTCTTACAATACAGTCATTTTCTTCCCCATTTTATACAA	Oy 601 TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTCATTCTTGTTATTTGTT 660		OY 481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA 540	OY 421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAATAACCAAAGTAACTAATCCACT 480	Qy 361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAAGACCAGCCATGTCTAGTG 420	OY 301 TTATTATTCTTTAGATATTATTTATTTTTGGAAAAATAACAAACTTATACTTTTGTGTA 360	QY 241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA 300	QY 181 CTGACCGAGGCCCATCAGACACCCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240	Db 121 CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT 180	Oy 61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAACTTCCACGGGTGCATGAT 120

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                                     Male tissue-preferred regulatory region and method Patent: WO 0160997-A 3 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Fraser, C.M., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Schubert, K., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
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3 (Dases 1 to 18828)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M. Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen,
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Chan,A.P., Pertea,G., Zheng,L., Cheung,F., Lee,D., Koo,H.,
Utterback,T.R., Feldblyum,T.V., Rabinowicz,P., Fraser,C.M.,
Schubert,K., SanMiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T.,
Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. a
                                                                                                                                                                                                    Direct Submission
Submitted (25-JAN-2005) The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850
On Jan 25, 2005 this sequence version replaced gi:57863105.
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Consortium for Maize Genomics -
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NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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                                                                                                               Contact: maize@tigr.org
                                                                                                                              Web site: http://www.tigr.org/tdb/tgi/maize/
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1 01	estimated_length=unknown	estimated length=unknown 34045134144		04000104099 estimated_length=unknown 03478 153577	a.	.966 ated_	.498 ated	.352 lated_	.28 <u>0</u>  ated_	a.	xref="taxon:4577" \ne="ZMMBBC0196I14"	organism="Zea mays" mol_type="genomic DNA" etrain="B73"	acion/Qualitiers 188283	33: contig of 3760 bp in	4: gap of unknown length 3: contig of 11079 bp in 3: gap of unknown length	gap of unknown length contig of 1639 bp in	16/405: contig of 5/20 bp in length 167505: gap of unknown length 171505: contig of 4000 bp in length	5: contig of 1009 bp in 5: gap of unknown length	6: contig of 1160 bp in 6: gap of unknown lengtl	6: contig of 5096 bp in 6: gap of unknown length	142904: gap of unknown length 154520: contig of 11616 bp in le 154620: gap of unknown length	134144: gap of unknown tength 142804: contig of 8660 bp in length	gap of unknown length	gap of unknown	contig of 5224 legap of unknown		1: contig of 46647 1: gap of unknown	49754: contig of 14494 bp in le 49854: gap of unknown length	0: gap of unknown length	gap of unknown	2213: CONTIG OF 2213 up in rength 2223: gap of unknown length 27064: Contig of 5731 hm in length	available and the	be updated with th
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prect Submission	Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Vassillev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Vassillev, A. and Zody, M. W. Wangan, Vonna G. Zainonn, T. Zenbek, L., Zimmer, A. and Zody, M.	ncer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,	yen.C. Nicol.R., Norbu.C., O'Connor.T., O'Donner.re, eil.D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N eil.D., Phunksa Pamasamv.H. Raymond.C. Retta.R., Rise,C.,	donald, P., Major, J., Manning, J., Matthews, C., McCarthy donald, P., Major, J., Manning, J., Mlenga, V., Murphy, T., Ndrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Ndrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Ndrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Ndrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Ndrim, J., Manning, J., Matthews, C., McCarthy	at,A., Karatas,A., Kells,C., Landers,T., Levine,R., at,A., Karatas,A., Kells,C., Landers,T., Levine,R., at,A., Karatas,A., Kells,C., MacLean,C.,	reira,P., Fitzderaid,M., Gage,D., Galagai,O., Galaga ham,L., Grand-Pierre;N., Hafez,N., Hagopian,D., Hagos 1 T Horton L. Hilme,W., Iliev,I., Johnson,R., Jones	z,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J.,	uslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cuslavkiy, L., Cock & Cornm B. Dearellano K.	(Dases 1 CO 186199) ren,B., Nusbaum,C., Lander,B., Abouelleil,A., Allen,N. ren, M. Barra,N. Bastien,V., Bloom,	ro -	Birren,B., Nusbaum,C., Lander,E., Butler,E., wing,K., Bnaitt,A.S. and Messing,J.	clade; Panicoideae; Andropogonaee; Zea.  1 (bases 1 to 186199)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Control of the	Zea mays	HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.	" ອິ	186199 bp DNA linear HTG 17-AUG-2004		 TAGCCCTA 35637	TAGCCCTA 916		алаттастттатттегтстттаталалападаласасттадалалапададттдссадас 908	TTTTTTAAGAGCTAGTTTGGCAACCTGTTTCTTTCAAGGATTTTGATTTTCTTAAGAG 3569 TTGTTTAAGAGCTAGTTTAGGAACCTGTTTTTAAAGGGATTTTATTTT	Conservative 0; Mismatches 23; Indels 2; Gaps	5.9%; Score 77.2; DB 14; Length 188 80.5%; Pred. No. 0.00021;	/escruated_rength=anvnown	/ estimated_testy	173245 173344 173245 173344	171506. 171605	167406167505 /estimated length=unknown	162086. 162185 /estimated_length=unknown	160977161076 /estimated length-unknown	159717159816

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Qor manually edited. This assembly was performed with Arachne (Genome Res. 2002 12: 177-189; Genome Res. 2003 13: 91-96). All trace files for this project are available at the NCBI trace repository
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Birren, B., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.ncbi.nlm.nih.gov/Traces/trace.fcgi?). An exact list of reads used in this assembly are available at http://www.broad.mit.edu/annotation/plants/maize/randomclones.html
provided by the submittor.

provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available and
by the ession number will be preserved.

the accession number will be preserved.

1 100617: contig of 100617 bp in length

100618 100717: gap of unknown length

100718 104730: contig of 4013 bp in length
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                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: 334_A_1
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                                                                                                    Submitted (24-FEB-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiriles: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 26, 2005 this sequence version replaced g1:60279457.
                  Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                 Danio rerio
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                                                                                                                                                                                                                                                                                                                                                      CR936840.2 GI:60302473
                                                                                                                                                                                                                                                                                                                                                                      CR936840
Center project name: zK9102:
                                                  Web site:
                                                                      Center code: SC
                                                                                     Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                 Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                       unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTTTCTTTTACTTTTAGGGCTAGTTTGGGAACCCTATTT-TTCTAAGAAATTTTCATTT
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ilarity 71.4%;
Conservative
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115204: gap of unknown length
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156396: gap of unknown length
179336: contig of 23440 bp in length
180136: gap of unknown length
180136: gap of unknown length
186199: contig of 6163 bp in length.
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Pred. No. 0.00023;
0; Mismatches 45; Indels 1;
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SEQUENCING IN PROGRESS ***,
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 153361 bases at least Q40
Consensus quality: 157330 bases at least Q30
Consensus quality: 158179 bases at least Q20
Insert size: 160416; sum-of-contigs
Insert size: 160313; 4.7% error; agarose-fp
Quality coverage: 6.55x in Q20 bases; sum-of-contigs Quality
coverage: 6.56x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/db_xref="taxon:7955"
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79168. .97393
                                                                                                                                                                                                                                                                                                                                    note="assembly_fragment:01299
fragment_chain:1"
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                                                                                                                                                                                                                                           note="assembly_fragment:00002
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ragment_chain:1"
                                                                                                                                               note="assembly_fragment:00606
ragment_chain:1"
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3: gap of 100 bp
3: contig of 8602 bp in length
3: gap of 100 bp
4: contig of 9840 bp in length
5: gap of 100 bp
4: contig of 23114 bp in length
6: gap of 100 bp
6: contig of 2237 bp in length
6: gap of 100 bp
7: contig of 100 bp
8: contig of 237 bp in length
8: gap of 100 bp
9: contig of 100 bp
1: contig of 100 bp
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         756 TGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25/69 bp DNA linear INV 21 Dictyostelium discoideum chromosome 2 map 5836255-5862024 AX4, complete sequence. AC117267 AC115597 AC117267.2 GI:42733680 HTG.
             Baumgart, C.
Direct Submission
                                                                                                                                                      Sequence and analysis of Nature 418 (6893), 79-85
                                                                                                                                                                                                                                           Dictyostelium discoideum
Dictyostelium discoideum
Dictyostelium discoideum
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 25769)
1 (bases 1 to 25769)
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                                                                                                                                                                                                                      Noegel, A.A.
                                                                he Dictyostelium Genome Sequencing Consortium (bases 1 to 25769)
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fragment_chain:1"
fragment_chain:1"
158891. 161616
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ragment_chain:1"
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ragment_chain:1"
17399. .158790
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INV 21-FEB-2004

FEATURES

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CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml
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                                                                                                                                                                                                                                                                                                                                                                KLAQNNKTTINIIGISGSHIDLGVIGKVSEQTNONITIHPLELAREIKKLTQNPMIA
TDVEMSICLHPTLEINKYDSKQGLSRVVKQFPNVNSLTDLTLLYSSNKRPTEFVQIYP
FQIQIKYTKLDGVRCLRVVSAQLQATPDFNTSTSNANISILAMAFTQQAAKIAQQQEY
MESRLHLKAATKLIRSLCAUTDEQMEEFYNFEVLREEMBAFLITCIKNKQQRVEKAATD
DEIQVFYKMKNVHKSFVEGGRKKDISRRKGEAEINKQYYNIKFT"
complement (5711 . 6796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGSGSGSSGTSGAQLSGTGYVINHQ"
join(2957. 3173,3272. 5583)
/note="GeneID exon scores (in ord.
24.88, 254.96 - GSCJ_ID dd_00753"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKYSNSNILLEQGEIPNKDSVEYVLSSPSTSSTTDGSKREBSIIIYCIDVSGSMGITT
EVPSLJGSEWVAAKGVKGASSGPSYISKLECVQSSITTMIDKLSIQYPNKRVVLVTFS
DEVMIYTQSUSVDGPIVIAGDKLEDPDQLIEIGRSMTYDKLFTASGSSBFLKAKIKSKL
EPVQSTALGPALLVSAAIASQKMLSEVVICTDGVPNVGLGAIEDLPLGPAQEFYEKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFFTLVRHTPRNTVYKVVVMGGGGVGKSAIIIQFIQNHFVEEYDPTIEDSYRKQVTIS
GLPPIGGSLNKKSSSSSSSSSSSGKTGLFNKIFSGKDKQPSPQQAASPSTIDRTGQI
STNRLEANVLSYSMSNLSKEVPLITGDCVYCQGCNVILSRFSNLVKTGDDSFTWKCEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mefftkyvyitsnidkpkewftqSemslitttdtiqksfvnnsg
ssssskgfgeavlldildtagqeeysamrdqyvrtgdcfmivfsidsrssfeevsqlk
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FSKQVIKSFLQNGYNIGIKSSKNTFIKIFENNKDKLFSSLPFFYLKNIAENQEFEDYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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ILSKSEWFRSLEYSSNKKVIFEVFDGFNHEYIENLDRIIKEFRENKVYGVDFSFSFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="GeneID exon scores (in order of location ranges):
23.68, 1.54, 15.75, 9.21, -4.75 - GSCJ_ID dd_03387"
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KNSNHWMMPSLKINQIINDNNNNISNINFVQIQSNSSSLSSSCSTYQSCPIEDEHIQE
                                                                                                                                              Hypothetical protein"
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/strain="AX4"
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                                                                                                                                                                                                                                                                                                   codon start=1
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                                                                                                                                                                                                                                            product="similar to Plasmodium
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                                                                                                                       translation="MSSRVKSLIERYNGINLTIEKSLSPRGLINTNINNNINNNNNNNN
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TQILFHLRLYNIHANKKVFLPFIQLVDYKFKGYLQSWYLNYHDDNDDDADEDSYDSDI
DDDDSYSDGGNCSSSGSSDIGSSNSINGISNSSSSILSELSHNIRVNSI
PEGLKSIEFEKEYNVIQDRLLPPSISSIRFSYGFNQRIAKGVISDNVISITFGDSFNQ
SLDGNWLFKQLKHLQFGHKFQQTIKMGQLFSSLTSLLDFRSYKGVIEIGSIPDSYKT
LDYKRNGCSNQESISINDIFKGSTTRLVDFSENQNIKANDISNYNLTSIHFGHENS
DIGIKSLPNSIREIKFGRAFDRDIKLCPSSITSIDFGNKFNRPLSMMTQTLTSIDFGS
KFNQIIPQGTFIHTKLKSLNFGYHFNQIIPADTLPFTLSLNLGGYNREITVKNDEYD
CYGISNKGGFGSNSSSNFCVGGTNNGLEMLKNTTSLKTLTLAYFRKIEVGDLPNSI
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/note="GenelD exon scores (in order of location ranges):
0.08, 32.32, 227.42 - GSCJ_ID dd_00726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Traibiation="MSSTIITPIATTTINNNSTINGIINSKTINETLEKNIKNIIPIS
PNAPTEKNIKGIIGNENNIKORKLINSDGVIPGKKNILETESKISMVSTTKHS
SSSSILAKNEYGIIGNGPNIVNNIKORKLINSDGVIPGKKNILETESKISTIDLESITATTIKI
KITDAFVAASSSSVKKTIDVILEFKSANTKRPIQIDIVENHQKEIVVPLSILETTPYN
NINNNINTRINSSGHTANGQKYPIFSPQISPFKIAYAQSSGTKTININNINNINTP
TKKANSNITTPOSINRNINTNSTSTTEQPUAIIDGATDSTINSSFKKTPLKETIDFRLA
ARQRQIDIGKMTAGYKNYIALVPKSKRKPTDPKTENKQVCSKRSWDGQIKKMRRQLH
ARQRQIDIGKMTAGYKNYIALVPKSKRKPTDPKTENKOVCSKRSWDGQIKKMRRQLH
/trainblation="metgedcnkitneeechkssecivinytdecgegkwacskgtfd
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TKNSCSSSGTSGSSSGTSGSSSGTTSGGSSSGTTSGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGGSSSGTTHCPEGYHCEKWNNDVATCLASTTGGTSLPGTSSGTAGVSSCLTT
LCPIGHICVEDSNGVKCVPNGGGTSGGSSSTCTSGGHPDPCRDVDCPDGFHCECKDGK
TAKCVPSPTTGSSSTSGGHPDPCKDVTCPDGFHCECKDGKTAKCVPSPTTGSSSTSGG
TNNPCSNVNCFDGFFYCEKKDGKTAKCVPSGFFQPFCVSLRCPPNHECRFNDQHQ
CCVKVHHDDRCSLRCPFHECKVDHNGKECCVRSGRPPPQHEKCNKRCPPGHECK
VDQHGKECCVVAHRPPPKCSLRCPPHHECRVNHFGEECCVKVHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPPKCSLRCPPHHECRVNHFGEECCVKVHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPPKCSLRCPPHHECRVNHFGEECCVKVHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPPKCSLRCPPHHECRVNHFGEECCVKVHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPPKCSLRCPPHHECRVNHFGEECCVKVHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPPKCSLRCPPHHECRVNHFGEECCVKVHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPKCSLRCPPHHECRVNHFGEECCVKVHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPKCSLRCPPHHECRVNHFGEECCVKVHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPKCSLRCPPHHECRVNHFGEECCVKVHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPKCSLRCPPHHECRVNHFGEECCVKVHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPKCSLRCPPHHECRVNHFGEECCVKVHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPKCSLRCPPHHECRVNHFGEECCVKVHDKCSLRCPPGHECK
VDQHGKECCVVAHRPPKCSLRCPPHHECRVNHFGEECCVKVHTGTBCCVCNHFGEECCVKVHTGTBCCVCNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCVKNHFGEECCV
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/protein_id="AAS38630.1"
/db_xref="GI:42733686"
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EKYLAWGSIEESIIKTNGTINKSIFEEFFYFGFTFKEIIL
DDYIFEKINSLIESIIKTNGTINKSIFEEFKFYGFTFWEIINEFQNFTHKESFQF
IINANSLWIKSSIDSRNISNSPINSRCSFNEYFEKRSSDASGDFILTISMIGIMDNYI
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/protein_id="AAS38629.1"
/db_xref="GI:42733685"
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23.29 - GSCJ_ID dd_00728"
/codon_start=1
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join(8924. .9076,9236. .10573)
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/note="GeneID exon scores (in order of
/.42, 136.56 - GSCU_ID dd_00727"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTIELIIDHYLKFLSSIETILKLYQNDQSTYQLLKQVFQNSNKILSGIYFAHKKSKRY
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/protein_id="AAS38628.1"
/db_xref="GI:42733684"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="similar to Dictyostellum discoideum (Slime mold). Spore coat protein SP87 precursor (PL3 protein)" /protein id="AAS38631.1" /db_xref="GI:42733687"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="similar to Dictyostelium
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kDa protein"
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RESULT 12
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Best Local
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217; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTATGACGITCAGATTTTTCTTTTTCATTCTTGTTATTTTGTTATTGTTTTTATATACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGAACAAGATTTAAAAAAAATAACCAAAGTAACTAATCCACTCGAAAGCTATCATGTAA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAGTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 АААТТАТТТАТТАААТТАТТТАААТТGATTTAATTGTTAACAATAAAAAAAACAAAATAAA 2571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAG
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                                                                                                                                                                                                                                                                                                              TTAAAAATTGGGTGTTTGAATGAAAATATTCTTTTAAATTTTTTCAGGAAATATCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTAAG
                                                                                                                                                           TTATTTTTTTTTTTTTTTTT 2829
                                                                                                                                                                                                                                  TATTTCTCTTTATAAAAT
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larity 49.4%;
Conservative
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/translation="MUNNUL.PQPYEPQSNNYCDCDDNENGNDSTLTIQPKPIAPSLPS
SQDPSPTISQINHWKYQLFKEFKEHNNIDSKMLCVQLSEFQISFKTATNTFDSWLN
SLWLPTGFKKLUDNHLKYQYIFFYSYRVNYNVEFSGFVTYDSKLNYNALYDKYGNTN
STYNNNYYNVNNNSLNNSNNADKNKKTITSTSATILNKENVELYNNGNNNNLNNKNS
EDIIKDKSIKWKVDGYITRTINRILLLACUSMDLLSDSIKNCMVSQFPFNNVIEK
EDIIKDKSIKWKVDGYITRTINRILLLACUSMDLLSDSINNCMVSQFPFNNVIEK
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SSSIVIKCEEQQQQQQQQQQQQQQQQQQQQQQGFLKSQEFPNLFKNKLYLKDDIS
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YTQNYFSTLVGNFBPFSKCKGDBLAIIDSFKVYNTSSYFLTFSRSSTNFLGSSSIGHL
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173.48 - GSCJ_ID dd_00724"
/codon_start=1
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ress)    Putative PREG1-like negative regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="GI:42733689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "HCAMKTVPIDKENCCEKVPVCYSNNPLLDGGHGFI
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3 (bäses I to 172293)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroll, A.C., Rohlfäng, T., Schubert, K., Bankjuel, P., Ma, J., Pontaroll, A.C., Rohlfäng, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
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AF034389 Plasmodium falciparum sexual stage antigen (s16) gene, promoter and partial cds. AF034389 AF034389.1 GI:3098290 AF034389.1 GI:3098290 Plasmodium falciparum (malaria parasite P. falciparum) Plasmodium falciparum Blaciparum Dlasmodium falciparum Blaciparum Conings, R. N. and Stunnenberg, H.G. Foolings, R	/estimated_length=unknown    5.5%; Score 71.6; DB 14; Length 201985;   Frity 76.9%; Pred. No. 0.0022;   Indels 1; Gaps 1;   Ga	/esclimated_length=unknown 155027. 155126 /estimated_length=unknown 156435. 156534 /estimated_length=unknown 17325. 173324 /estimated_length=unknown 174859. 174958 /estimated_length=unknown 182701. 188800 /estimated_length=unknown 185731. 185972 /estimated_length=unknown	/estimated_length=unknown 6521965318 /estimated_length=unknown 7877578874 restimated_length=unknown 8779887897 /estimated_length=unknown 9446494563 /estimated_length=unknown 121762121861 /estimated_length=unknown 121637124736 /estimated_length=unknown 131030133129 /estimated_length=unknown 131030133129 /estimated_length=unknown 131030133129 /estimated_length=unknown 1310301331839 /estimated_length=unknown 136839 /estimated_length=unknown 14660146959 /estimated_length=unknown 152970153069 /estimated_length=unknown 152970153069

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 CAAGATTTAAAAAAATAACCAAAGTAACTAATCCACTCGAAAGCTATCATGTAATGTTTA
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Dechering, K.J., Kaan, A.M. and Konings, R.N.H.
Direct Submission
Submitted (12-NOV-1997) Molecular Biology, University of Nijmegen,
Toernooiveld 1, Nijmegen 6525 ED, The Netherlands
                                                                                                                                                                                                                              CGTTCAGATTTTTCTTTTTCATTCTTTATTTTGTTATTGTTTTTTATTATATACATTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                             AATATTATCCTATGATAATAAAGCTATTGTGGAAATTATATTTTATGGAAAATATAATAT
                                                                                                                                                                                                                                                                                                          AAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAGCATATTTCGAAAGAGACAA 563
CCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTATTTCTCTAGATTAGTAAAAAGGGA 104
                                                                        TTCCCAATAAATTACAATCACTGTGTATAATTATTTGGCCAGCCCCATAAATTATTTAAA 983
                                                                                                  CTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCTAGAATGTT
                                                                                                                                                     TTTATTTATTTTATATATATAATTTTTTTTTTAAATTTTAAATTCATATATTTTAATTT
                                                                                                                                                                              TTTTCAGTATAAAAAGTATTTAACGGAAATATGTAGAATGGAAAAGAAGAATTTGGTATG
                                                                                                                                                                                                                                                                                                                                                            ATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAGCTATGA 623
                                                 Conservative
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537. .>713
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537. .710
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711. .>713
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/mol type="genomic DNA"
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Pred. No. 0.0063;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escalante,R., Wessels,D., Soll,D. and Loomis,W.F.
Direct Submission
Submitted (27-JAN-1997) Department of Biology, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 3576)
Escalante,R., Wessels,D., Soll,D.R. and Loomis,W.F.
Chemotaxis to CAMP and slug migration in Dictyostelium both depend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum MigA (migA) gene, U86962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9307972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on migA,
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Biol. Cell 8 (9),
                                                                                              951. .1289
/gene="migA"
/note="encodes
                                                                                                                                                                                                                                                                                                                                                           /function="essential for slug migration"
/note="N-terminus of this protein is similar to other BTB
domain proteins, such as the Mus musculus and human zinc
finger proteins encoded by GenBank Accession Numbers
/114556 and L16896, respectively"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    join(884. .2899,2998. .3423)
/gene="migA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....(<884. .2899,2998. .>3423)
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                                                                                     LEIYGELCETNPNPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       map="4.25"
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  domain; similar
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Query Match 5.4%; Score 71.2; D
Best Local Similarity 47.2%; Pred. No. 0.00
Matches 217; Conservative 0; Mismatches
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                        832 TTTGATTTTTTCAAAAAAAATTAGTTTATTTTCTCTTTAT 871
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712 TTTTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGT 771
                                                                                                                                                                                                                                                                                                                                                                     532 CTTAAAAAACAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          852 TATTTATTATTATTATTATTACAATTTTGTTTTTGTATAAAAAAATAAAAATAAAAAA 793
                                                                                                                                                                                                                                                                             TIGITATITTTGTTATTTTTAAATAATTATTTATTTATACAATAAAATACTTTAAACACAAC 553
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Number U01333"
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replace="pbsrl external plasmid, approximately 4 kb"
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Search completed: March 5, 2006, 21:55:27 Job time : 5725.47 secs

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Title: Perfect score: Sequence:

US-10-713-381-1\_COPY\_1\_1311 1311

Run on:

OM nucleic - nucleic search, using sw model

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

EST:\*

gb\_est1:\*
gb\_est2:\*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

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Total number of hits satisfying chosen parameters:
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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CG224225 OG1AG08TV
CC656939 OGMDQ20TV
CC656939 OGMDQ20TV
CG252571 OG4BB05TC
CT235046 ZMMBB0057
CZ295176 ZMMBB0057
CZ295176 ZMMBB0053
CG048704 PUILO19TB
CG414922 ZMMBB0029
CC439901 PUIRO15TB
CG384247 PUHOC67TB
CG103452 PUJBE19TB
CG082135 PUFGX12TD
CC630219 CGUCGS3TH
CC630210 CGUCGS3TH
CC630210 CGUCGS3TH
CC433618 PUHHP17TD
AL175696 Tetraodon
BZ816381 PUFBA86TD
CL997678 ZMSHE60D
CCG201774 PUICH24TB
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                                                                         Query Match
Best Local Similarity
Matches 908; Conserva
        9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5943
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i (bases 1 to 963)
whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Numberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGW0Q20TV
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays
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Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                             ilarity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                               /organism="Zea mays"
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CC003943
CL996481
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CC385762
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CC613918
                                                                                                                 Score 908; DB 9; Length 963; Pred. No. 9.6e-180;
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CG333925 OGOAD14TV
CG034985 PUIGRERSBTB
BZ797976 PUBEPCTB
CC430754 PUHEPCTB
CC430754 PUHEPCTB
CC435780 PUHSNO3TD
BZ78478 PUFHV09TD
BZ78478 FUFHV09TD
CC620594 OGUCC26TV
CC613318 OGJAGB8TV
CC613318 OGJAGB8TV
BZ676889 PUBIG1TD
CC003943 PUDJN65TD
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Result No.

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Query Match

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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
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1 (bases 1 to 915)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGLAGO8TH
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/note="Vector: pBCSK-; Site 1: HincII;
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/strain="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 687)
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Location/Qualifiers
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/clone lib="ZM 0.7_1.5_KB"
/clone="Vector: pBcSK: Site 1: HincII; 0.7-1.5
/note="Vector: pBcSK: Site DNA library"
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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JOURNAL
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CL235046
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CG252571/c
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Best Local Sim
Matches 125;
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                                                            237
                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@ti
                                                                                                                                                                                                                                                                                                                                                                                                           Class: methylation filtered.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CG252571.1 GI:34154661
                                                                                                                                                                                                                                  h 7.3%;
Similarity 80.1%;
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                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                      /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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1249 CTCCCAAACATCCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTG 1308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387 CAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTA
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                                                                                                                                                                356 reacacacecercirerecerireredareredecerrececerciearedadecea
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                                                                             296 TAAGGCACCTGTCGGAGAACCCCATTAAAGGCCTTTCGGATGGCCCACGGGACAT-CGGGG
                                                                                                                       195 TCAGACACCTTTCGGGACACCCCATCAAGGGCCTTTCGGATGGCCCACGAGACGTATCGGG
                     255 TCGTGGTGATCCAGGGGATATATGTCCCCCACAATC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG252571 715 bp DNA linear GSS 25-AU GG48B3C7C ZM 0.7_1.5 KB Zea mays genomic clone ZMMBMa0809B10, genomic survey sequence.
CG252571 CG252571
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regregrejacecegegeararerarececeacaace 202
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(clone="ZMMBMa0809B10"
(clone="Ib="ZM.0.7 1.5 KB"
(note="Vector: pBCSK-; Site 1: HincII; 0."
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                 Score 96; DB 10; Length 715;
Pred. No. 1.5e-09;
0; Mismatches 30; Indels
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SOURCE
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AUTHORS
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AUTHORS
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VERSION
KEYWORDS
SOURCE
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CZ295176
LOCUS
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Best Local :
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                                                                                                                    ORGANISM
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ZMMBBb0575001r ZMMBBb (HindIII) Zea mays genomic clone
ZMMBBb0575001 3', genomic survey sequence.
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Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronz Zohovetz,V., Fuke,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c)
                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea
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Tel: 732 445 3801
Fax: 732 445 5735
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The Plant Genome Initiative at Rutgers, Waksman Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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GSS.
                               1 (bases 1 to 860)
Bharti, A.K., Nelson, A.B.,
                                                                                                                                                                                     survey sequence.
CZ295176
                                                                                                                                                                                                                    CZ295176
ZMMBF0063M20f ZMMBF Zea
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
Construction, Sequencing
                 and Messing, J.
                                                                                                                  Zea таув
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Similarity 78.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                          GGATATATGTCCCCCACAAT 289
                                                                                                                                                                                                                                                                                                                                                                                                                  GACACCCATCAAGGGCCTTTCGGATGGCCCCACGAGACGTATCGGGTCGTGGTGATCCAGG
                                                                                                                                                                                                                                                                                                                                                                                      GTGGCCCATCAAGTGCCTTTCGGATGGTCCACGGGATGTATCCGGGCCGTGTGACCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCGCCTTTCTTGGATACCGGCGGTTCCCCGTCTGATTGAGGCCCATCCAGCACCTTTTGG
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:4577"
/db xref="taxon:4575001"
/clone="ZMMBBb0575001"
/lab host="E. coli DH10B"
/clone lib="ZMMBBb (HindIII)"
/clone lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/cultivar="B73"
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Pred. No. 1e-08;
0; Mismatches
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 and
                               Young, S.,
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genomic
 Characterization
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ic clone
                                 Keizer, G.,
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                                                                                                                                                                                                                      linear GSS
ZMMBF0063M20
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 of
a
                               Zohovetz, V.,
 Fosmid Library
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5', genomic
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                                  Fuks, G
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RESULT 7
CG048704
LOCUS
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AUTHORS
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VERSION
KEYWORDS
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Best Local Similarity
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                                                                                                                                                                 TITLE
                                                                                                                                                  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the B73 Maize (
Unpublished (2005)
Contact: Bharti, A
                                              9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                 Unpublished (2003)
Other_GSSs: PUILO19TD
                                                                                                                                                                                      1 (bases 1 to 814)
Whitelaw C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw C.A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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CG048704
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PUILO19TB ZM_0.6_1.0_KB Zea mays
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Seq primer: Fos_F
Class: fosmid ends.
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Fax: 732 445 5735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute,
                                                                                                                                                                                                                                                                                               Zea mays
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Class: sheared
               Seq primer: TR
                              Email: whitelaw@tigr.org
                                                                                                                 Contact: Cathy Whitelaw
                                                                                                                                                                 Maize Genomics Consortium
                                                                                                                                                                                 Bennetzen, J
                                                                                                                                                                                                                                                                                                                    Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GANATICCITTGCTANTGATTGAGGGGGGAGAGAATTCGTAACTATCCA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTGG
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/clone="ZMMBF0063M20"
/lab_host="EPI100-T1"
/clone_lib="ZMMBF"
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/mol_type="genomic DNA"
/cultivar="B73"
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/note="Vector: pEpiFOS-5; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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Pred. No. 1.7e-08;
0; Mismatches 85;
                                                                                  Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                 DNA linear
genomic clone ZMM
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; Poales; Poaceae; PACCAD
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                                                                                  20850,
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ZMMBTa0611C13,
                                                                                    USA
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                 Zea mays
                                                                                                                                                                                                                   Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                       Plate: 0290 row:
Seq primer: Ml3r
                                                                                                    BACKWARD: Ml3r
                                                                                                                                                            Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                               Sequencing of the maize genome 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                      clade; Panicoideae; Andropogoneae; Zea.
                                                             Class: BAC ends.
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                                                                                                                                                                                                       iological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               730
                                                                                                                                             rwing@genome.arizona.edu
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/clone="ZMMBTa0611C13"
/clone lib="ZM 0.6 1.0 KB"
/clone="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0
CoT selected genomic DNA library"
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'mol_type="genomic D'
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'strain="B73"
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/organism="Zea mays"
/mol_type="genomic D
                                          Location/Qualifiers
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                                                                                                                                                                                                        P.O. Box 210088, Tucson, AZ
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Best Local Similarity
Matches 126; Conserv
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                                     787
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Zea mays
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Unpublished (2003)
Other GSSs: PUHRV15TD Contact: Cathy Whitelaw
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Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                              Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                  Email: whitelaw@tigr.org
                                                                  Conservative
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/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                    location/Qualifiers
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/clone_lib="ZMMBBb"
/note="Vector: pBelbBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
Score 87.8; DB 10
Pred. No. 7.8e-08;
0; Mismatches 47
                                DB 10; Length 754;
    Indels
    0
    Gaps
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899 GTTGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAAT 941
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241 ATCTTTCTAATGACTAGTTTGGGAACCTTATTT-TCTCACGGGATTTTTATTTTTTCAAT 183
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CC439901
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1 (bases 1 to 950)
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                                   ATTTTTTAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTGATTTTTTCAAA 846
                                                                                                                                                                                                                         /clone_lib="ZM_0.6_1.0 KB"
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CoT selected genomic DNA library"
                                                                                                     Score 86.8; DB 9;
Pred. No. 1.3e-07;
D; Mismatches 47;
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RESULT 11
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Matches 131; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: whitelaw@tigr.org
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/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                         organism="Zea mays"
/mol_type="genomic D
/strain="B73"
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0; Mismatches
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genomic survey s
CC400574
CC400574.1 GI::
GSS.
Zea mays
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Zea mays
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CC400575 CC400575.1 GI:30880665
GSS.
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(bases 1 to 797)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                          REVIEWED THE SM 0.6 1.0 KB Zea may8 genomic clone ZMMBTa480L01.
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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/clone="lib="ZM_0.6_1.0_KB"
/clone="Vector: pCR4_TOPO; Site_1:
/note="Vector: pCR4_TOPO; Core selected genomic_DNA_library"
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/strain="B73"
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                                                    GI:30880664
                                                                                   sequence
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Pred. No. 1.4e-07;
0; Mismatches 109;
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ORGANISM

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CG103452
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Other_GSSs: PUHLU61TD
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                                                                             Ekkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 471)
                                                                                                                                                            Zea mays
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GSS.
                                      Whitelaw, C.A., Quackenbush, J., Va
Resnick, A., Fraser, C.M., Yuan, Y.,
                                                                                                                                                                               Zea mays
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telaw,C.A., Quackenbush,J.,
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0
CoT selected genomic DNA library"
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/mol_type="genomic DNA"
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Pred. No. 1.4e-07;
0; Mismatches 109;
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                                      n Aken,S., Utterback,T.,
San Miguel,P., Ma,J. and
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Best Local Similarity
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9712 Medical Center Drive,
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Other_GSSs: PUJBE19TD
Contact: Cathy Whitelaw
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1 (bases 1 to 765)
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Resnick, A., Fraser, C.M.,
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                                                                        Class: sheared ends.
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                                                                                                                                                                                   12 Medical Center Drive,
1: 301-838-5843
x: 301-838-0208
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/mol_type="genomic DNA"
/strain="B73"
/db_xref=":
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/clone_lib="ZM_0.6_1.0_KB"
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CoT selected genomic DNA library"
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/mol_type="genomic DNA"
/strain="B73"
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San Miguel,P., Ma,J. and
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Class: methylation filtered.
Location/Qualifiers
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CC630219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2002)
Other_GSSs: OGUCG53TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
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                                                           ATCTTTCTAATGACTAGTTTGGGAACCTTATTT-TCTCACGGGATTTTTATTTTTTCAAT
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methylation filtered genomic DNA library"
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CoT selected genomic DNA library"
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Search completed: March 6, 2006, 01:57:38 Job time : 6193.32 secs

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Sequence 2, Appli
Sequence 34, Appl
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Sequence 11, Appl
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Sequence 26, Appl
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APPLICANT: Cigan, Andrew M.

APPLICANT: Cox, Timothy W.

APPLICANT: Hexshey, Howard P.

APPLICANT: Hexshey, Howard P.

APPLICANT: Wu, Yongzhong

ITITLE OF INVENTION: Methods of Using Same

ITITLE OF INVENTION: Methods of Using Same

ITITLE OF INVENTION: Methods of Using Same

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CURRENT APPLICATION NUMBER: US/11/014,071

CURRENT APPLICATION NUMBER: US/13/044,071

FRIOR APPLICATION NUMBER: 0004-12-16

PRIOR APPLICATION NUMBER: 0005-12-16

PRIOR APPLICATION NUMBER: 0005-12-16

PRIOR APPLICATION NUMBER: 0005-12-16

PRIOR APPLICATION NUMBER: 0005-12-16
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TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: promoter
LOCATION: (1)...(1092)
OTHER INFORMATION: P95
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Best Local Similarity 57.3
Matches 142; Conservative
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6 US-09-925-065A-206150
8 US-10-925-065A-206150
8 US-10-240-708-2
6 US-09-925-065A-206149
8 US-10-240-708-7
12 US-11-011-332A-96
7 US-10-330-773-242
7 US-10-330-773-243
7 US-10-330-773-835
8 US-10-240-708-13
12 US-11-1121-086-25
8 US-10-240-708-13
12 US-11-121-086-25
8 US-10-240-708-13
12 US-11-121-086-25
8 US-10-240-708-13
13 US-10-240-708-13
14 US-11-011-332A-90
15 US-10-330-773-963
17 US-11-011-332A-91
18 US-09-925-065A-714069
18 US-09-925-065A-714069
18 US-11-011-332A-77
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US-10-240-708-36
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PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
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LENGTH: 9347
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Best Local Similarity
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Disgnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REPERENCE: 5013.101.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/240,708 CURRENT FILING DATE: 2002-10-03
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                       8710 TAATATTTTTTGTTGTTTTTATGAATGTAATGTTTTTTTCGTATTGTTTTTTGTTTTGTT
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TAAGATTTTATTTTGTT
                                 AAAATTAGTTTATTTT 863
                                                                          ATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTCAAA
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8846
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Pred. No. 0.64;
0; Mismatches 162; Indels
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US-10-330-773-534

Sequence 534, Application US/10330773

Publication No. US20060040262A1

GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
ITITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001300

CURRENT APPLICATION NUMBER: US/10/330,773

CURRENT FILING DATE: 2002-12-27

NUMBER OF SEQ ID NOS: 981

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 254336
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT PILLING DATE: 2001-08-08
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
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; ORGANISM: Homo sapiens
US-10-330-773-534
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                                                                                                                                                                                                                                                                                                                                   Sequence 54272, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCATGTCGTAGATTCTCGATTCAAAAATCTTTCTGATTTTTTTAAGAGCTAGTTTTGGCAA 811 ·
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0; Mismatches 214;
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Pred. No. 3.
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APPLICATION NUMBER:

60/289,846

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; ORGANISM: Homo sapiens
US-09-925-065A-54272
                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-925-065A-803046
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                                                                                                                                                                                                                                                             SEQ ID NO 803046
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Best Local
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NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 54272
                                                                                                                                          Query Match
Best Local
                                                                                                                      Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 803046, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2001-0
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 108827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: Wang, David G.
ITLE OF INVENTION: Identification and Mapping of Single
ITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/250,092 FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/261,766 FILING DATE: 2001-01-16
                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    835 GATTTTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGA 890
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670 ATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATA 729
                                                                                     610
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Similarity 51.0%;
                                                                                                                                      Similarity
                                                     Conservative
                                                                                                                                                                                                                                                                                                                2001-05-09
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                                                                                                                                      4.18;
                                                                                                                                                                                                                                                                                                                                US 60/289,846
                                                                                                                      Score 53.6; DE Pred. No. 1.7; 1; Mismatches
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                                                                                                                                                        DB 6;
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US-10-240-708-73/c
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Best Local
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CURRENT APPLICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
CURRENT FILING DATE: 0007/ED01/03971
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PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITTLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITTLE OF INVENTION: by Assessing DNA Methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5152
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-04-06
APPLICATION NUMBER: DE 10019058.8
FILING DATE: 2000-04-06
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FILING DATE: 2000-06-30
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                                                               4137 CTACAATCCCAACTACTCAAAAATCTCAAACAAAAAATAACTTAAACCCAAAAATTCAA
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                                                                                                  665
                                                                                                                                                                                                                485
724 ACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTT
                                                                                                                                                                             605 ATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTTATTTG 664
                                                                                                                                                                                                                                                                                                                                                                                                           425 CTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACTCGAA 484
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                                                                                                TITITATATACATITT-CTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATG 723
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No. US20050282157A1
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Pred. No. 3;
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APPLICANT: DIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE: 5013.1012
CURRENT EPELICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 63
             RESULT 8
US-10-995-561-13314/c
US-equence 13314, Application US/10995561
; Publication No. US20050272054A1
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US-10-240-708-63
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US-10-240-708-63
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Best Local S
Matches 140
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GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTTATTTGTTTATAT 673
                                                                                                                                                     TAGTTTATTTTCTCTTTATAAAATAGA 879
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ilarity 52.4%;
Conservative
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Pred. No. 3.3;
0; Mismatches
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PELICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                                                                            Sequence 803045, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13314
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Best Local Similarity
                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827, 135
CURRENT FILLING DATE: 2001-08-08
CURRENT FILLING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
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CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG REI
TITLE OF INVENTION: DETECTION AND USES THEREOF
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ORGANISM: Homo sapiens
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OTHER INFORMATION: n =
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                                                                                                                                                    ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-240-708-11
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; ORGANISM: Homo sapiens
US-09-925-065A-803045
                                                                         Query Match
Best Local Simi
Matches 218;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 803045
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Publication No. US20050282157A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
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Best Local
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SEQ ID NO 11
LENGTH: 6317
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR THING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION UNMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
                                                                                                                                                                                    TYPE: DNA
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
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2030 АСGАТААТААААААААААААААААААААТААААААСТСАААААССТАТАТАААААССА 1971
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                                    424 ACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACTCGA 483
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                                                                                             Similarity
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                                                                         0; Mismatches
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Pred. No. 3.3;
1; Mismatches 141; Indels
                                                                                             Score 51.6;
Pred. No. 7
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                                                                                                             Length 6317;
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RESULT 11
US-10-330-773-242/c
US-10-330-773-242/c
Sequence 242, Application US/10330773
Publication No. US20060040262A1
GENERAL INFORMATION:
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; NAME/KEY: misc feature
; LOCATION: (1)...(355211)
; OTHER INFORMATION: n = A,T,C'or G
US-10-330-773-242
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Best Local Similarity 46.1%;
Matches 211; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 242
LENGTH: 355211
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CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
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ORGANISM: Homo sapiens
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                                      ATTCATTAATATATTAATTAACAATACTCTTTCAATTTCTCTATATATTTAAAAATATTTC 1611
      TCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAGTCATTTTTAT 742
                                                                      AATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAGCTATG
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Pred. No. 1
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LENGTH: 173602
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NICCLEIC ACID PROBES AND NUCLEIC .
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 50/567,570
PRIOR APPLICATION NUMBER: 50/567,570
PRIOR APPLICATION NUMBER: 50/567,570
PRIOR APPLICATION NUMBER: 50/567,570
PRIOR APPLICATION OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
136778
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Local Similarity 45.5%;
38 219; Conservarium
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                                                                                                                TATATTATATATTATATAATATTTTATATATATATGTTATATATTTTTATATATATATATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51.4;
Pred. No. 1
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Best Local :
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RESULT 14
US-09-925-065A-667262
; Sequence 667262, Application US/09925065A
; Publication No. US20040181048A1
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human (
PILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-10-330-773-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: NOVel Compositions and Methods in
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 687411
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (1)...(68741
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Conservative
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Pred. No. 25;
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RESULT 15

US-09-925-065A-667263, Application US/09925065A

Sequence 667263, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

ITILE OF INVENTION: Identification and Mapping of Single

ITILE OF INVENTION: Nuclectide Polymorphisms in the Human Gence

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/250,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER: OF SEQ ID NOS: 957086
SEQ ID NO 667262
SEQ ID NO 667262
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; ORGANISM: Homo sapiens
US-09-925-065A-667262
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Best Local :
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NUMBER: US 60/261,766
: 2001-01-16
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Matches 214
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOPTWARE: FASTSEQ for Windows Version 4.0
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FTH: 677
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214; Conserv
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909 TAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTAT
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